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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res 8, 205-213, 2010.

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AC2079

A;Accession: AC2079

A;Accession: Draininary

A;Molecule type: DNA
                                                                                                                                                                                                 A,Residues: 1-853 «KUR»
A,Cross-references: GB:BA000019; PIDN:BAB73884.1; PID:g17131276; GSPDB:GN00179
A,Expendental source: strain PCC 7120
C,Genetics:
A,Gene: alr2185
C,Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-deoxyxylulose-5-phosphate synthase BH2779 [imported] - Bacillus halodurans (strain C-1
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cipate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
Cipate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
Cipates 51 Takami, M.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4117-4131, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: CB3997
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-629 <STC>
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable ferric siderophore receptor protein NMA0575 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Species: OS-May-2000 #sequence_revision OS-May-2000 #text_change O2-Feb-2001 C;Accession: D81976 #sequence_revision OS-May-2000 #text_change O2-Feb-2001 F;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Asture 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556; PMID:10761919
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C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CABB3866.1; PID:g737931
A;Experimental source: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                           Length 853;
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100.0%; Pred. No. 0.014;
ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2%; Score 9; DB 2;
100.0%; Pred. No. 1.5;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: BH2779
C;Superfamily: hypothetical protein C2814
                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.5
Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity luv.
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A; Residues: 1-725 < PAR>
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C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 31-Tax-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81038
R;Tettellin, H: Saunders, N.J.; Heidelberg, J.; Jefffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A;Reference number: A81000; MUD:20175755; PMID:10710307
A;Accession: B81038
A;Status: preliminary
A;Molecule type: DNA
A;Reseduces: 1-708 <-TET>
A;Cross-references: GB:AE002532; GB:AE002098; NID:G7227078; PIDN:AAF42164.1; PID:g722708
A;Experimental source: serogroup B, strain MCS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TonB-dependent receptor NMB1829 [imported] - Neisseria meningitidis (strain MCS8 serogro
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C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AC2079
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probable glucose-1
sensor histidine k
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RNA-binding protei
hypothetical prote
                                                       protein-tyrosine/s
                                                                                protein-tyrosine/s
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hypothetical prote
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                                                                                                                          B71146
D87645
A87410
T08262
S53494
T00873
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AG1316
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G75007
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A;Gene: NMB1829
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R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TonB-dependent receptor NMB1882 [imported] - Neisseria meningitidis (strain MC58 C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SPBC19C7.07c - fission yeast (Schizosaccharomyces pombo
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
59K transcription activator -
                                                                                                                                                                                                                                                                                                A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: Z21881
A;Accession: T39813
                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-725 <TET>
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                                                                                                                                                                                                                             A; Map position:
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                                                                                                                                                                                                                                                                                                                A;Residues: 1-284 <LYN>
                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                                                                                                                                                                                                            Gene: SPDB:SPBC19C7.07c
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Similarity 100.0%;
8; Conservative (
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9; Conserv
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100.0%; Pr/
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Library, June 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2%; Score 9; DB:
100.0%; Pred. No. 1.0
ive 0; Mismatches
equine herpesvirus 1 (strain Ab4p)
                                                                                                                                                                       Score 8; ; Pred. No.
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; Dougherty,
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strain MC58.
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ferrioxamine B receptor precursor [imported] - Salmonella enterica subsp. e
(;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AC0547
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C;Superfamily: varicella-zoster virus gene 63 protein; RING finger C;Superfamily: varicella-zoster virus gene 63 protein; RING finger C;Keywords: DNA binding; transcription regulation; zinc finger F;4-52/Domain: RING finger homology <RNG>
F;8-46/Region: zinc finger C3HC4 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable alpha-isopropyl malate synthase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Datc: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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A;Title: The DNA sequence of equine herpesvirus-1.
A;Reference number: A41831; MUID:92295566; PMID:1318606
A;Contents: annotation; possible protein-coding frames
A;Note: neither amino acid nor nucleotide sequence is given
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: leuA
C;Superfamily: 2-isopropylmalate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18032.1; PID:g296013-A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: G70794
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C;Date: 30-Sep_1992 #sequence_revision 30-Sep-1992 #text_change 17-Mar-2000
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100.0%; Pred. No.
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us-09-889-267-2.oligo.rpr

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-813 <POO>
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S; Arkenbauer, R.G.; Quan, H.N.
J. Bacteriol. 176, 307-319, 1994
A; Pitle: FptA, the Fe(III) Pycohell receptor of Pseudomonas aeruginosa: a phenolate sid A; Fitle: FptA, the Fe(III) Pycohell receptor of Pseudomonas aeruginosa: a phenolate sid A; Fitle: FptA, the Fe(III) Pycohell receptor of Pseudomonas aeruginosa: phenolate sid A; Fitle: Preliminary
A; Folecule type: DNA
A; Frose-references: GB:U03161; NID:9454352; FIDN:AAC43213.1; PID:9454353
A; Cross-references: GB:U03161; NID:9454352; FIDN:AAC43213.1; PID:9454353
A; Cross-references: GB:U03161; NID:9454352; FIDN:AAC43213.1; PID:9454353
A; Cross-references: GB:U03161; NID:9454352; FIDN:AAC43213.1; PID:9454353
A; Fitle: Complete genome sequence of Fseudomonas aeruginosa PA01, an opportunistic pathoraces of Species of Complete genome sequence of Fseudomonas aeruginosa PA01, an opportunistic pathoraces and A; Frein PA01
A; Fatus: preliminary
A; Reference number: A82950; MUID:20437337; PMID:10984643
A; Residues: 1-720 65T0>
A; Cross-references: GB:AE004839; GB:AE004091; NID:99950434; PIDN:AAG07609.1; GSPDB:GNO01
A; Fitle: Complete genome sequence: strain PA01
C; Generics:
A; Generics:
C; Ge
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L., T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; A; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A; Reference number: AB0502; PMID:11677608
A; Accession: AC0547
A; Statuus: preliminary
A; Molecule type: DNA
A; Residues: 1-696 < PAR>
A; Residues: 1-696 < PAR>
A; Crosser references: GB:AL513382; PIDN:CAD08819.1; PID:g16501633; GSPDB:GN00176
C; Genetics:
A; Gene: STY0396
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AE0187
probable iron-siderophore receptor YPO1537 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AE0187
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
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Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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100.0%; Pred. No. 18;
:ive 0; Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
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54 PQSVSIIT 61
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A;Gene: YPO1537
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo
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CAccession: Ad601; S54000; P67227
R;Poole, K.; Neshat, S.; Krebes, K.; Heinrichs, D.E.
J. Bacteriol. 175, 4597-4604, 1993
A;Title: Cloning and nucleotide sequence analysis of the ferripyoverdine receptor gene f)
A;Reference number: A40601; MUID:93328663; PMID:8335619
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUD:21470413; PMID:11586360
A;Accession: AB0187
A;Accession: AB0187
A;Accession: Apolls?
A;Residue: 1753 < KUR>
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C;Genetics:
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Cibate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jan-2000
Cipaccession: T30917
Sibavidson, S.; Rohlfing, T.
submitted to the EMBL Data Library, August 1999
A; Reference number: 220934
A; Reference number: 220934
A; Retence num
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A;Introns: 44/3; 146/3; 224/1; 343/2; 422/3; 494/3; 579/3; 668/3; 709/3
A;Note: D1007.15
C;Superfamily: Caenorhabditis elegans hypothetical protein D1007.15
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llarity 100.0%; Pred. No. 20;
Conservative 0; Mismatches
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submitted to the EMBL Data Library, March 1994
A;Reference number: S53998
A;Accession: S54000
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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protein D1007.15 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
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A;Residues: 1-715;'Y',717-744,'YN',745-747,'S',749-813 <LAM>
A;Residues: 1-715;'Y',717-744,'YN',745-747,'S',749-813 <LAM>
R;Cross-references: EMBL:U07359; NID:g1633044; PIDN:AAB60199.1; PID:g466459
R;McMorran, B.J.; Merriman, M.E.; Rombel, I.T.; Lamont, I.L.
                                          A; Note: published errata appeared A; Accession: E87759
                                                                A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                     R;anonymous, The C. elegans Sequencing Consortium Science 282, 2012-2018, 1998
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C; Superfamily:
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A; Residues: 1-815 <STO>
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Nature 406, 959-964, 2000
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83345
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C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 176, 55-59, 1996
A;Title: Characterisation of the pvdE gene which is required A;Reference number; JC5090; MUID:97075909; PMID:8918232
A;Accession: PC4227
                                                                                                                                                                                              C; Accession: E87759
                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE004666; GB:AE004091; NID:g9948438; PIDN:AAG05786.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:U07359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-49 <MCM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ferripyoverdine receptor PA2398 [imported] - Pseudomonas aeruginosa (strain
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Matches
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                          Status: preliminary
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type: DNA
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8; Conser
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8; Conserv
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ilarity 100.0%;
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100.0%; Pred. No.
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0; Mismatches
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A.; Larbig,
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K.; Lim,
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                                                                                                                                                     A;Gene:
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Best Local S
Matches 8
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460 GLSLIGG 466
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mes 8; Conser
                                                                Similarity 7; Conserv
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Nakazaki, N.; Shimpo, S.; Sugimoro, P., Aller.

Nakazaki, N.; Shimpo, P., Aller.

Nakazaki, Na
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Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: A89959
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C;Superfamily: Caenorhabditis elegans hypothetical
                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DAA
A;Residues: 1-78 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74126.1; PID:g17131519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, 
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
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A;Residues: 1-1274 <KUR>
A;Cross-references: GB:BA000018; PID:g13701536; PIDN:BAB42830.1;
A;Experimental source: strain N315
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C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89959
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1.0%; Score 7; llarity 100.0%; Pred. No. Conservative 0; Mismatc
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100.0%; Pred. No. 30
ive 0; Mismatches
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30;
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    Indels
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Conserved hypothetical protein Atul525 [imported] - Agrobacterium tumefaciens (strain C5 (Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 (SAccession: AD2764 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L., Rage, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 ** State C5 (State C5) ** State C5 (State C5)
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C;Date: 20-Apr-2001
C;Date: 20-Apr
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A,Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Accession: AD2764
A,Status: preliminary
A,Status: preliminary
A,Rolecule type: DNA
A,Residues: 1-108 «KUR»
A,Residues: 1-108 «KUR»
A,Exerimental source: GBAR008688, PIDN:AAL42530.1; PID:g17739951; GSPDB:GN00186
                                     A,Accession: C97545
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87316.1; PID:g15156613; GSPDB:GN00169
C;Genetics:
A;Gene: AGR C 2812
A;Map position: circular chromosome
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1.0%; Score 7; DB 2.
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches
A; Reference number: A97359; PMID:11743194
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A;Gene: ML2274
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Chioredoxin TC0826 [imported] - Chlamydia trachomatis Mopn
CjSpecies: Chlamydia muridarum, Chlamydia trachomatis Mopn
CjSpecies: Chlamydia muridarum, Chlamydia trachomatis Mopn
CjAccession: C81660
CjAccession: C81660
RjRead, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Ree. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Recession: C81660
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
A;Accession: C81660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 - TET>
A;Cross-references: GB:AE002349; GB:AE002160; NID:g7190851; PIDN:AAF39627.1; PID:g719085
A;Experimental source: strain Nigg (WoPn)
C;Genetics:
A;Genetics:
A;Geneti
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res, 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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C97545
C) Protein AGR C 2812 [imported] - Agrobacterium tumefaciens (strain C58, Cere C) Proteins and Tumefaciens (strain C58, Cere C) Proteins: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens (species: Agrobacterium tumefaciens C) Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C; Accession: C97545
C; Accession: C97545
A; Liu, F; Wollam, C; Allinger, M; Doughty, D; Scott, C; Lappas, C; Markelz, B.; Science 294, 2323-2328, 2001
A; Liu, F; Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
                                                                                                                                                                                                                                                                                                                                                         C; Species: Nostoc sp. A; Note: Nostoc sp. A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 5.0 bate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: AC186 R; Nanko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
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A;Molecule type: DNA
A;Residues: 1-84 <KUR>
A;Residues: 1-84 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB72594.1; PID:g17129982; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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26 GLSLIGG
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A; Map position:
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A;Residues: 1-127 <OLI>
A;Residues: 1-127 <OLI>
A;Cross-references: EMBL:Z99296; PIDN:CAB16594.1; GSPDB:GN00066; SPDB:SPAC3H5.10
A;Experimental source: strain 972h-; cosmid c3H5
                                                                                                                                                                                                                                                                                                                                                                    R;Oliver, K.; Harris, D.; Wood, V.; Barrell, B.G.; submitted to the EMBL Data Library, September 1996 A;Reference number: Z21809 A;Accession: T38756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60s ribosomal protein L32 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
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A;Residues: 1-123 <TIM
A;Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47150.1; PID:g45390
A;Cross-references: EMBL:X66592; NID:g45388; PIDN:CAA47150.1; PID:g45390
A;Coss. reference, P.; Hickey, M.J.; Bradman, S.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Tille: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Residues: 1-123 <STO3
A;Cross-references: GB:AE004919; GB:AE004091; NID:g9951346; PIDN:AAG08440.1; GSPDB:GN001
A;Experimental source: strain PAO1
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A;Title: Cloning and molecular analysis of the poly(3-hydroxyalkanoic acid) gene locus
A;Reference number: S29303; MUID:93011120; PMID:1396693
A;Accession: S29304
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les 7; Conserv
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                                                                                                                                  rat ribosomal protein L32
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                           1.0%; Score 7; DB:
llarity 100.0%; Pred. No. 48
Conservative 0; Mismatches
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o. 47;
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                        A; Reference number: S71253
A; Accession: S71256
                                                                         R;Grellet, F.; Cooke, R.; Laudie, M.; Raynal, M.; Delseny, M. submitted to the EMBL Data Library, October 1995
                                                                                                                             C; Accession: S71256
                                                                                                                                                   ribosomal protein L27a, cytosolic - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text
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A;Molecule type: mRNA
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: A84120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-127 <PUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1998
A;Reference number: Z21863
A;Accession: T39562
                                                                                                                                                                         A; Gene: BH3761
                                                                                                                                                                                                                A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07480.1; GSPDB:GN00 A;Experimental source: strain C-125
                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-130 <STO>
                                                                                                                                                                                                                                                                                                                           A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84120
                                                                                                                                                                                                                                                                                                                                                                    R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 2
C; Superfamily: rat ribosomal protein L32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60S ribosomal protein L32 - fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP synthase protein
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Matches
                                                                                    Matches
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                                      632 NLWTTYQ 638
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                                                                             Local Similarity nes 7; Conserv
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47 NLWITYO
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                                                                                  Conservative
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53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH3761 [imported] - Bacillus halodurans (strain C-125)
                                                                                                         100.0%;
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k; Pred. No. 48;
0; Mismatches
                                                                                  0;
                                                                                                      Score 7; Pred. No.
                                                                                  Mismatches
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                                                                                                         49;
                                                                                  <u>0</u>
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#text\_change

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A;Cross-references: EMBL:Z72625; NID:g1322642; PIDN:CAA96808.1; PID:g1322643; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 30
877384
hypothetical protein sll1455 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: 877384
R;Kaneko, T:; Sato, S:; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okwura, S.; Shimpo, S:; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA, Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA17487.1; PID:g165256.
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein sll1455
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AH3359
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A;Molecule type: DNA
A;Residues: 1-165 <MUS
A;Cross-references: GB:AE008917; PIDN:AAL52043.1; PID:g17982810; GSPDB:GN00190
A;Experimental source: strain 16M
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                                                                                         A;Gene: SGD:CYH2; RPL29; MIPS:YGL103w
A;Cross-references: SGD:S0003071; MIPS:YGL103w
A;Tross-references: SGD:S0003071; MIPS:YGL103w
A;Introns: 17/1
A;Introns: 17/1
C;Superfamily: rat ribosomal protein L27a
C;Keywords: protein biosynthesis; ribosome
F;2-149/Product: ribosomal protein L27a.e #status experimental <MAT>
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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llarity 100.0%; Pred. No. 57;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Query Match
1.0%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches
                                  A;Experimental source: strain S288C C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-155 < KAN>
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription regulator (imported) - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23. Amz-2001 #sequence_revision 23. Mar-2001 #text_change 01. Mar-2002
C;Accession: C86732
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malaxme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: C86732
A;Accession: C86732
A;Molecule type: DNA
A;Residues: 1-148 <STO>
A;Cross-references: GB:AE005176; PID:g12723787; PIDN:AAK04957.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: ahrC
C;Superfamily: Escherichia coli arginine repressor argR
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REBULL 25
REBULL 26
C. Species: Saccharomyces cerevisiae
C. Species: Saccharomyces cerevisiae
C. Species: Saccharomyces cerevisiae
C. Species: Saccharomyces cerevisiae
C. Recession: A02782; 835696; 564110
R. Kaeufer, N. F.; Fried, H.M.; Schwindinger, W. F.; Jasin, M.; Warner, J.R.
Nucleic Acids Res. 11, 3123-3135, 1983
A. Title: Cycloheximide resistance in yeast: the gene and its protein.
A. Reference number: A02782; MUID:83220732; PMID:6304624
A. Recession: A02782
A. MOID:83220732; PMID:6304624
A. Recession: A02782
A. MOID:83220732; PMID:6304624
A. Recession: A02782
A. MOID:83220732; PMID:6304624
A. Residues: 1-149 - KMD.
A. Residues: 1-149 - KMD.
A. Residues: 1-149 - KMD.
A. Residues: 1-16 - SCA.
A. MOID:87194763; PMID:3553182
A. MOID:87194763; PMID:3553182
A. MOID:87194763; PMID:3553182
A. MOID:87194763; PMID:372481; PIDN:AAA35002.1; PID:9553140
A. Residues: 1-16 - SCA.
B. Riseger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
Bubmitted to the Protein Sequence Database, May 1996
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-149 - KIE>
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                              A;Cross-references: EMBL:X91959; NID:g1107486; PIDN:CAA63025.1; PID:g1107487
C;Superfamily: rat ribosomal protein L27a
C;Keywords: protein biosynthesis; ribosome
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1.0%; Score 7; DB 2; Length 148; Best Local Similarity 100.0%; Pred. No. 55; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                              Length 146
                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                              1.0%; Score 7; DB 2;
100.0%; Pred. No. 54;
cive 0; Mismatches
                                                                                                                                                              Query Match 1.04
Best Local Similarity 100.0
Matches 7; Conservative
A; Residues: 1-146 <GRE>
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DB 2;

Score 7;

1.0%;

Query Match

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C;Accession: C86231
R;Theologis, A.; Ecker, J.R.; Palm, Chin, C.W.; Chung, M.K.; Conn, L.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
                                                                                           hypothetical protein [imported] - Arabidopsis tha C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; I Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid A;Reference number: Z17011; MUID:97271300; PMID:9128251
A;Accession: T10313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: F83062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
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A; Residues: 1-173 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PA4661 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                  Conway,
                                      C.J.; Federspiel, N.A.;
Conway, A.B.; Conway, A.
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                                    iel, N.A.; Kaul, S.; White, O.; Conway, A.R.; Creasy, T.H.; Dev
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A.; Larbig,
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <STO>
                                                                                                                          A; Map position: 1
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C;Genetics:
                                         Matches
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200
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                                         Conservative
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Maiti, R.; Ma
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H+-transporting two-sector ATPase (EC 3.6.3.14) delta chain - N;Alternate names: hydrogen ion-transporting ATPase delta chai Escherichia coli (strain 01-Mar-2002

A;Title: The atp operon: nucleotide sequence of the promoter A;Reference number: A93732; MUID:82059437; PMID:6272190 A;Accession: A93732 N;Alternate names: hydrogen ion-transporting ATPase delta chain C;Species: Escherichia coli C;Species: Bscherichia coli C;Date: 18-Dec-1981 #sequence\_revision 02-Apr-1982 #text\_change C;Accession: A93732; A90101; T41274; H65176; T45005; A01031 R;Gay, N.J.; Walker, J.E. R;Gay, N.J.; Walker, J.E. Nucleic Apids Res. 9, 3919-3926, 1981 and the genes for the membr

A; Molecule type: DNA A; Residues: 1-177 <GAY> A;Cross-references: GB:V00264; GB:X00771; NID:g41023; PIDN:CAA23517.1; PID:g41028

R;Mabuchi, K.; Kanazawa, H.; Kayano, T.; Futai, M. Biochem. Biophys. Res. Commun. 102, 172-179, 1981
A;Title: Nucleotide sequence of the gene coding for the A;Reference number: A90101; MUID:82068433; PMID:6458296
A;Accession: A90101 delta subunit of proton-transloc

A;Molecule type: DNA A;Residues: 1-81,'D',83-177 <MAB> A;Residues: 1-81,'D',83-177 <MAB> `~~~~~~~farences: GB:M12212; GB:M12213; NID:g145396; PIDN:AAA20044.1; PID:g145398

R;Kanazawa, H.; Futai, M.
Ann. N. Y. Acad. Sci. 402, 45-64, 1982
A,Title: Structure and function of H+-ATPase: What we har A;Reference number: I41271; MUID:83176724; PMID:6301339
A;Accession: I41274 have learned from Escherichia

GB/EMBL/DDBJ

A;Status: preliminary; translated from A;Molecule type: DNA

A;Residues: 1-177 <RES>

A;Cross-references: GB:M25464; NID:g146318; PIDN:AAA83872.1; PID:g146322 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.

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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H65176 K-12.

A; Status: preliminary; nucleic acid sequence not shown; translation not

A; Molecule type: DNA A; Residues: 1-177 < BLAT>

PIDN:AAC76758.1; PID:g1790173;

Meyenburg,

A;Cross-references: GB:AE000450; GB:U00096; NID:g1790166; A;Experimental source: strain K-12, substrain MG1655 R;Nielsen, J.; Hansen, F.G.; Hoppe, J.; Friedl, P.; Von Me MO1. Gen. Genet. 184, 33-39, 1981 A;Title: The nuclotide sequence of the atp genes coding f A;Reference number: Z22893; MUID:82147764; PMID:6278247 A;Accession: T45005 for the F-0 subunits ā ά a

A;Status: preliminary; translated from GB/EMBL/DDBJ

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H-transporting two-sector ATPase (EC 3.6.3.14) delta chain [imported] - Yersinia pestis C;Species: Yersinia Holden: M:C:Delta Holden, M:C:
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Jun-2002
C;Accession: E91213
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91213
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hypothetical protein VCA0195 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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C;Superfamily: H+-transporting ATP synthase delta chain
C;Keywords: hydrolase
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C;Superfamily: H+-transporting ATP synthase delta chain
C;Keywords: hydrolase
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Matches 7; Conservative 0; Mismatches
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A; Residues: 1-177 < KUR>
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F86059
H+transporting two-sector ArPase delta chain [similarity] - Escherichia coli (strain O15 C; Species: Escherichia coli
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C; Accession: F86059
R; Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: F86059
A; Accession: F86059
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-177 <STO>
A; Residues: 1-177 <STO>
A; Residues: 1-177 <STO>
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: atpH
C; Superfamily: H+-transporting ATP synthase delta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arussa Arussa delta chain [imported] - Salmonella enterica subsp. enterica serovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi G;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002 C;Accession: AC0954
R;Parkhill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T; Connerton, P; Coronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; PMID:11677608
A;Accession: AC0954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-177 <PAR>A;Residues: 1-177 <PAR>A;CGenetics:
C;Genetics:
A;Genetics:
A;Genetics:
A;Gene: STY3910
C;Superfamily: H+-transporting ATP synthase delta chain
                                                                                                                                         A Gene: atpH; uncH
A,Gene: atpH; uncH
A,Map position: 84 min
C;Complex: this is one of the five chains of the enzymatic component (F1) of the ATPase
C;Superfamily: H+transporting ATP synthase delta chain
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex
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                               A,Residues: 1-177 <NIE>
A,Cross-references: EMBL:V00266; NID:g41031; PIDN:CAA23524.1; PID:g41034
C,Genetics:
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Similarity 100.0%; Pred. No. 64;
7; Conservative 0; Mismatches
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1.0%; Score 7; DB 2,
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches
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Best Local Similarity
Matches 7; Conserv
A;Molecule type: DNA
A;Residues: 1-177 <NIE>
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on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Readune, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
A; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus A; Accession: E95072
A; Accession: E95072
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 53/3; 80/3
A;Note: F17A8.180
C;Superfamily: Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F17A8.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82490
                                                                                                                                                                  C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: B95072
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peter
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Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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A;Experimental source: cultivar Columbia;
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A; Residues: 1-191 <BEV>
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A; Accession: T04031
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A;Experimental source: serogroup
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A; Residues: 1-182 <HEI>
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                                                                                                                                                                                                                                                 nitroreductase family protein [imported] - Streptococcus
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Sequence Database,
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100.0%; Pred. No.
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100.0%; Pred. No.
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O1; strain N16961; biotype El Tor
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Radune, D.; Holtzapple,
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R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: B97940
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-201 <KUR>
A;Residues: 1-201 <KUR>
A;Residues: 1-201 <KUR>
                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-208 <STO>
A;Cross-references: GB:AE005176; PID:g12725039; PIDN:AAK06092.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
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A;Cross-references: GB:AE005672; PIDN:AAK74774.1; PID:g14972098; GSPDB:GN00164; TIGR:SP4.
A;Experimental source: strain TIGR4
                                                                                                                                                                                                              A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: B86874
                                                                                                                                                                                                                                                                       R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                                                                                                           hypothetical protein yuhE [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: B86874
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C;Keywords:
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RESULT 45
AG2841
outer membrane protein omp [imported] - Agrobacterium tumefaciens (atrain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AG2841
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ater, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Accession: AG2841
A;Accession: AG2841
A;Accession: AG2841
A;Molecule type: DNA
A;Residues: 1-209 ckUR>
A;Consolue type: Ony
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Search completed: December 18, 2002, 06:59:29 Job time: 40.351 sece

117 GSVRGRV 123

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Run 3

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Maximum DB
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VG08_BPMU
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R27C_ARATH
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  drosophila
                                                                      mycoplasma
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In Acids Res. 284.317-4331 (2000).

In Catalyzes the acyloin condensation reaction between C acroms 2 and 3 of pyruvate and glyceraldebyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).

In Acyloid Acyloid Acyloid Acyloid Sphots and Sphosphate and Glyceraldebyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2).

COPACTOR: Thiamine pyrophosphate (By similarity).

In COPACTOR: Thiamine pyrophosphate (By similarity).

PATHWAY: Nonmevalonate terpenoid blosynthesis pathway; first step.

PATHWAY: Blosynthetic pathway to thiamine and pyridoxol; first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBŪNIT: Homodimer (By similarity).
SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY. DXS SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.;
             P40482
Q9hn24
P98198
P47563
P23129
P23129
P95759
                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2001 (Rel. 41, Last annotation update)
1-Geoxy-D-xylulose 5-phosphate synthase (EC 4.1.3.37) (1-6cxy-2002)
DXS OR BH2779
Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                      629 AA
                                                                                                                                                                                                                                                                     ALIGNMENTS
AACT_DROME
SC24_YEAST
SYA_HALN1
SECA_SYNY3
A8B2_HUMAN
                                                                                           SEA1 MYCLE
SECA STRGR
DIDE2 YEAST
CHTC YEAST
SECA STRCO
PMAS ARATH
SECA SYNDY
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MYCTU
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InterPro; IPR00360; Transketolase.
Pfam; PF02779; transket pyr; 1.
Pfam; PF02779; transketolase_c; 1.
TIGRFAMs; TIGNE0204; dxs; 1.
PROSTIE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                   Y321
                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Q9K971;
16-OCT-2001 (
16-OCT-2001 (
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DXS_BACHD
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May B.J., Zhang Q., Li L.L., Pauetian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                Gaps
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Pasteurella.
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                                                                 Length 629
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Lyase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete
SEQUENCE 629 AA; 69279 MW; 7B5909B2F427CIIE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA9F9C64442C7BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-DNA HYBRIDS SPECIFICALLY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: MANGANESE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: BELONGS TO THE RNASE HII FAMILY.
                                                               1.2%; Score 9; DB 1;
100.0%; Pred. No. 0.79;
                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
RIPE OR PM1998.
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100.0%; Pred. No. 3...
0; Mismatches
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BY SIMILARITY.
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Pfam; PP01351; RNase HII; I.
Hydrolase; Nuclease; Endonuclease; Mang
ACT_SITE 16 16 BY SIMILAN
ACT_SITE 108 108 BY SIMILAN
ACT_SITE 126 126 BY SIMILAN
ACT_SITE 126 BY SIMILAN
ACT_SITE 126 BY SIMILAN
ACT_SITE 126 BY SIMILAN
SEQUENCE 197 AA; 21589 WW; CAASPSPGC
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ICPO_HSVEB
ID ICPO_HSVEB
STANDARD;
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AC P28950;
DT 01-DEC-1992 (Rel. 24, Created)
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HSSP; Q57599; 1EKE.
                                                                                100.08;
                                                                                                9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=747;
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8
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-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
-i- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lyon
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Viruses; dsDNA viruses, no RNA stac
Alphaherpesvirinae; Varicellovirus
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Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
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PDB; 1CHC; 30-APR-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Mol. Biol
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16-OCT-2001
                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
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 Local Similarity hes 8; Conserv
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A sequence of equine herpesvirus-1.
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PS50089; ZF_RING_2; 1.
ption regulation; Trans
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047718; PubMed=8263911; 0.N., Milner A
                                                                      Conservative (
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                                                                        58629 MW;
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Last
                 1.1%; Score 8;
100.0%; Pred. No.
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Trans-acting
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RNA stage; Herpesviridae;
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annotation update)
al protein ICP0.
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   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residues and secondary structure virus protein family.";
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                 DB 1;
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L outstation -
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P96420; 069677;
30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYCTU
                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                              laboratory strains.";
Submitted (APR-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
2-isopropylmalate synthase (EC 4.1.3.12) (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase).
LEUA OR RV3710 OR MT3813 OR MTV025.058.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Alland D., Eieen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               rieischmann R.D., Alland D., Eisen Peterson J., DeBoy R., Dodson R., C Kolonay J.F., Nelson W.C., Umayam I Delbhar R. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=H37Rv;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1773;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Putative Mycobacterium synthase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                  Whole genome comparison of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
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                                                                                                                                                                                                                                                                                     FUNCTION: Catalyzes the condensation of the acetyl group of acetyl-COA with 3-methyl-2-oxobutanoate (2-oxobisovalerate) to for 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).

CATALYTIC ACTIVITY: 3-carboxy-3-hydroxy-4-methylpentanoate + COA acetyl-COA + 3-methyl-2-oxobutanoate + H(2)0.
                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE SYNTHASE FAMILY. LEUA 2 SUBFAMILY. CAUTION: Ref.1 sequence differs from that shown
                                                                                                                                                                                                                                                                  PATHWAY:
                                                                                                                                                                         in positions 49 and 77.
                                                                                                                                                                                                                                                     SUBUNIT: Homotetramer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bacteria; Actinobacteria (class); Actinobacteridae;
Corynebacterineae; Mycobacteriaceae; Mycobacterium
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tuberculosis alpha-isopropyl malate
                                                                                                                                                                                                                                                     (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases.
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                                                 . Usage by and for commercial http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                    HOMOCITRATE
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                                                                                                                                       collaboration
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U88526; AAB48096.1; ALT\_FRAME

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352
368
702 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=287;
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P42512;
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CONFLICT
SEQUENCE
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MEDLINE=95370139; PubMed=7642488;
MEDLINE=95370139; PubMed=7642488;
Tsoliss R.M., Baumler A.J., Stojiljkovic I., Heffron F.;
Fur regulon of Salmonella typhimurium: identification of new iron-regulated genes.";
J. Bacteriol. 177:4628-4637(1995).
-! FUNCTION: FERRIOXAMINE BINDING AND UPTAKE, IN ASSOCIATION WITH THE TONE PROTEIN (BY SIMILARITY). MAY PLAY A ROLE IN INTESTINAL COLONIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LTZ / SGSC1112 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
COUTENDY L., PORWOllik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SL1344;
BDDLINE-929203118; PubMed=10103258;
Kingsley R.A., Reissbrodt R., Rabsch W., Ketley J.M., Tsolis R.M.,
Kingsley R.A., Reissbrodt R., Rabsch W., Ketley J.M., Tsolis R.M.,
Everest P., Dougan G., Baeumler A.J., Roberts M., Williams P.H.;
"Ferrioxamine-mediated iron(III) utilization by Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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                                                                                                                                                                                                                                        533 TTASLR -> NRPA (IN REF. 1).
544 AAR -> RHARTALN (IN REF. 1).
70113 MW; 881A9AAEA7F8FB71 CRC64;
                                                                                                                                                                                                                                                                                                                          Length 644;
                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                      Tuberculist; Rv3710; -.
Tuberculist; Rv3710; -.
InterPro; IRR002034; AIPM/Hcit_synth.
InterPro; IRR00891; HMGL-like.
Pfam; PF00682; HMGL-like.
TIGRFAMB; TIGR00970; leuA_yeast; 1.
PROSITE; PS00815; AIPM HOMOCIT_SYNTH 1; 1.
PROSITE; PS00816; AIPM_HOMOCIT_SYNTH 2; 1.
Leucine biosynthesis; Lyase; Complete proteome.
DOMAIN
                                                                                                                                                                                                                                                                                                                        1.1%; Score 8; DB 1;
100.0%; Pred. No. 8.8;
tive 0; Mismatches
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appl. Environ. Microbiol. 65:1610-1618(1999).
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AL022121; CAA18032.1; -.
AE007178; AAK48181.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrioxamine B receptor precursor FOXA OR STW0364.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                       644 AA;
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Best Local Similarity
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                                         MT3813;
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Q56145;
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STRAIN=ATCC 15692 / PAO1;
STRAIN=ATCC 15692 / PAO1;
MEDLINE=2043737; Pubmed=10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltery L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Spiencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406:359-964 (2000).
-!- FUNCTION: HIGH-AFFINITY OUTER MEMBRANE RECEPTOR REQUIRED FOR THE TRANSPORT OF FE(III)-PYOCHELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phenolate siderophore receptor homologous to hydroxamate siderophore
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BDLINES-4411363; PubMed=8288523;
Ankenbauer R.G., Quan H.N.;
"FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a
                                                                                                                                                                                                                                                                                                                                                                                                    Stydene; Sci0646; foxA.
Stydene; Sci0646; foxA.
InterPro; IPR00513; TonB boxC.
BROSITE; PS00430; TONB DEPRNDENT REC 1; FALSE NEG.
PROSITE; PS01156; TONB DEPENDENT REC 2; FALSE NEG.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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249 MAYP -> SPYL (IN REF. 2).
255 G -> R (IN REF. 2).
279 F -> S (IN REF. 2).
352 A -> P (IN REF. 2).
354 HALLVGI -> SSSAGGD (IN REF. 7).
374 HALLVGI -> SSSAGGD CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                       EMBL, AE008712; AAL19318.1; -. EMBL, AF060876; AAC15464.1; -. EMBL; U62282; AAB04552.1; -. HSSP; P06971; 1BYS.
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P48632; Q51339;
01-FEB-1996 (Rel. 33, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
             "Complete genome sequence of Pseudomonas aeruginosa opportunistic pathogen.";
Nature 406:959-964(2000).
                                                     MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Pinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=ATCC 15692
                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ferripyoverdine receptor precursor. FPVA OR PA2398.
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Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                                                                           Poole K., Neshat S., Krebes K., Heinrichs D.E.; "Cloning and nuclectide sequence analysis of the receptor gene fpvA of Pseudomonas aeruginosa."; Bacteriol. 175:4597-4604(1993).
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TE; PS01156; TONB_DEPENDENT_REC_2; 1.
membrane; Iron transport; Transport; Signal; Receptor;
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SIGNAL
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MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
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EMBL; U07359; AAB60199.1; -.
EMBL; AE004666; AAG05786.1; -.
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                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                   Nucleic Acids Res. 28:1397-1406(2000).

-- FUNCTION: Participates in various redox reactions through the reversible oxidation of its active center dithiol to a disulfide and catalyzes dithiol-disulfide exchange reactions.
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Bacteria; Chlamydiales;
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15-JUN-2002
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Pfam; PF00593; TonB_boxC; 1.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; TonB_box; Signal; Receptor;
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INDUCTION: BY THE SIDEROPHORE, PYOVERDINE, AND UNDER STARVATION CONDITIONS.
STARVATION CONDITIONS.
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR P CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-16 IS
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Mood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Squros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Books K., Brown D., Brown S., Chillingworth T., Churcher C.M., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A dentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., A dames K., Jones L., Jones M., Leather S., McDonald S., McLean J., Amoney P., Munde S., Mungall K., Murphy L., Niblett D., Odell C., Andrew R., Jones L., Jones L., Gual M.A., Rabbinowitsch E., Oliver K., O'Neil S., Pearson D., Quall M.A., Rabbinowitsch E., Antherford K., Rutter S., Saunders R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Welton J., Simmonds M., Squares R., Schaefer M., Muleller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Antichen I., Vanstreafs E., Reaben J., Grymonprez B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Andle R., Much S., Lucas M., Rochet M., Gallardin C., Morre K., Hurst S.M., Lucas M., Rochet M., Galllardin C., Morre K., Hurst S.M., Cerrutti L., Lowe T., McCombie W.R., Parnstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Parnstrong J., Forsburg S.L., R., Parnstrong J., Forsburg S.L., Morron S., Armstrong J., Forsburg S.L., Morron S., Armstrong J., Forsburg S.L., Morron S., Marnstrong J., Rochet M., Shapakowski G.V., Waster B., Narwer B., Narwe
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                                                                                                                                                                 TIGR; TC0826; ...
InterPro; IPR000063; Thiored.
InterPro; IPR000065; Lhiored. 1.
PRINTS; PR00421; THIOREDOXIN.
TIGREPAMS; TIGR01068; thioredoxin; 1.
TIGRSTE; PS00194; THIOREDOXIN; 1.
Redox-active center; Electron transport; Complete proteome. DISULFID 28 31 REDOX-ACTIVE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                          Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetacese,
                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNC-2002 (Rel. 41, Last annotation update)
62 ribosomal protein L32-A.
RPL32A OR SPAC3HS.10
                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 7; DB 1
100.0%; Pred. No. 20;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21848401; PubMed=11859360;
                                                                                                                        EMBL; AE002349; AAF39627.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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NCBI TaxID=4896;
                                                                                                                                                P80579; 1QUW.
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Kawamukai M.;

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MEDLINE-21848401; PubMed=11859360;

Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squored V., Gwilliam R., Harlan D., Basham D., Boward S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

R. Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gontles S., Goble A., Hamlin N., Harris D., Hidagon G.,

And Holroyd S., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

And Holroyd S., Moules M., Leather S., McDonald S., McLean J.,

And Holroyd S., Horneby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

And Holroyd S., Moules M., Leather S., McDonald S., McLean J.,

And Holroyd S., Moules M., Leather S., McDonald S., McLean J.,

And Holroyd S., Moules M., Saunders D., Seeger K., Sharp S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Berzym K., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

Golfeau A., Cadleu E., Jimenez J., Sanchez M., Galzon A., Thode G.,

Londs M., Rochet M., Gaillardin C., Tallada V.A., Galzon A., Thode G.,

Boninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Certutti L., Lowe T., McCombie W.R.,

Bapakovski G.V., Ussery D., Barrell B.G., Nurse P.,

"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- MISCELLANEOUS: THERE ARE TWO GENES FOR L32 IN S.POMBE.
-!- SIMILARITY: BELONGS TO THE L32E FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.0%; Score 7; DB 1; Length 127; Best Local Similarity 100.0%; Pred. No. 24; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 AA; 14458 MW; 4BBB3CEB2E359E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
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15-DEC-1998 (Rel. 37, Last sequence update)
15-UDC-2002 (Rel. 41, Last annotation update)
62 ribosomal protein L32-B.
RPL32B OR SPBC16C6.11.
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                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                      EMBL; AB000914; BAA19212.1; -.
InterPro; IPR001515; Ribosomal_L32E.
Probom; PD003823; Ribosomal_L32e; 1.
Probom; PD003823; Ribosomal_L32E; 1.
PROSITE; PS00580; RIBOSOMAL_L32E; 1.
Ribosomal protein; Multigene family.
                                                                                                                                                                                                                                                                                                  EMBL; Z99296; CAB16594.1; -.
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042935;
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R32B_SCHPO
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RESULT 11
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Best Local S
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                             Query Match
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16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EWBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Morgan G., Hatfull G., Hendrix R.;
"Genome of bacteriophage Mu and comparison with the Haemophilus influenzae Mu-like prophage FluMu.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                          Hypothetical SEQUENCE 1
                                                                                    EMBL; M64097; AAA32391.1; -. EMBL; AF083977; AAF01134.1; -.
                                                                                                                                entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            Phage Mu, pp.277-296, Cold Spring Harbor Laboratory Press
New York (1987).
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Priess H., Brauer B., Schmidt C., Kamp D.;

"Sequence of the left end of Mu.";

(In) Symonds N., Toussaint A., van de Putte P., Howe M.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, Mu-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal protein; Multigene family SEQUENCE 127 AA; 14445 MW; 01490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01655; Ribosomal L32e; 1.
ProDom; PD003823; Ribosomal L32E; 1.
PROSITE; PS00580; RIBOSOMAL L32E; PALSE NEG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriophage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNKKTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001515; Ribosomal_L32E.
                                                          il protein
139 AA; :
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Md.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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LONGS TO THE L32E FAMILY OF RIBOSOMAL PROTEINS.
                                                          16310 MW;
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             100.0%;
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100.0%; Pred. No.
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               Score 7;; Pred. No.
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RX Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA Theologis A., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Chung M.K., Conn L., Conway A.B., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Hinter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced SSP consortium (Salk/Stanford/PGEC)."; SSP consortium (Salk/Stanford/PGEC).";
                                                                   EMBL; AC005292; AAF86998.1; --
EMBL; AF349525; AAK15572.1; --
EMBL; AF34716; AAG40067.1; --
EMBL; AF410280; AAK95266.1; --
EMBL; Z26208; CAA81190.1; --
                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-UUN-2002 (Rel. 4), Last annotation update) 605 ribosomal protein L27a-B. RPL27AB OR AT1023290 OR F26F24.13 OR F26F24_23. Arabidopsis thaliana (Mouse-ear cress).
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           Pfam; PF00256; L15; 1.
PROSITE; PS00475; RIBOSOMAL_L15; FALSE_NEG.
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15-JUN-2002 (Rel.
608 ribosomal prot
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15-JUN-2002
                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1993) to -!- SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                                   Hofte H.;
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WEDLINE=21016719; PubMed=11130712;

WEDLINE=21016719; PubMed=11130712;

WEDLINE=21016719; PubMed=11130712;

WEDLINE=21016719; PubMed=11130712;

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

White O., Alonso J., Altafi H., Cheuk R.F., Chin C.W.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fuji C.Y.,

A. And Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

A. Langin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

Militscher J., Miranda M., Nguyen M., Neoney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraeer C.M., Venter J.C., Davis R.W.;

"Lerizar C. and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
60S ribosomal protein L27a-C.
RPL27AC OR ATIG70600 OR F24J13.17 OR F5A18.22.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. Columbia;
MEDLINE=97336304; PubMed=9193080;
MEDLINE=97336304; PubMed=9193080;
COOKE R., Raynal M., Laudie M., Delseny M.;
"Identification of members of gene families in Arabidopsis thaliana by contig construction from partial cDNA sequences: 106 genes encoding 50 cytoplasmic ribosomal proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia; Asyana M., Grellet F., Delseny M.; Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
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                                                                     DB 1; Length 146; 27;
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3 4 TA -> DG (IN REF. 3).

31 G -> V (IN REF. 3).

139 139 G -> C (IN REF. 3).

146 AA; 16292 MW; 0CA6C019D8BIA565 CRC64;
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MEDLINE=87199.763; PubMed=3553182;
Schwindinger W.F., Warner J.R.
"Transcriptional elements of the yeast ribosomal protein gene CYH2.";
J. Biol. Chem. 262:5690-5695(1987).
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Underwood M.R., Fried H.M.;
"Characterization of nuclear localizing sequences derived from yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-83220732; PubMed=6304624;
Kaufer N.F., Fried H.M., Schwindinger W.F., Jasin M., Warner J.R.;
"Cyclobeximide resistence in yeast: the gene and its protein.";
Nucleic Acids Res. 11:3123-3135(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
60S ribosomal protein L28 (L27A) (L29) (YL24) (RP62).
RPL28 OR CYH2 OR YGL103W.
Saccharomyces cerevisiae (Baker, 8 yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetia; Saccharomyces.
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                                                                                                                                                                                                                                                                                                             Length 146;
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100.0%; Pred. No. 27;
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PROSITE; PS00475; RIBOSOMAL_L15; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
send an email to license@isb-sib.ch)
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                                                                                                          EMBL; Z17767; CAA79059.1; -. InterPro; IPR001196; Ribosomal_L15.
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                                                                               EMBL; AC011663; AAG52338.1;
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                                               EMBL; X91959; CAA63025.1;
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EMBO J. 9:91-99(1990).
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010299;
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01-NOV-1997
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
60S ribosomal protein L77a (L29).
Erysiphe graminis (subsp. hordei) (Grass mildew).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
NCBI TaxID=62688;
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PIR; A02782; R6
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE L15P FAMILY OF RIBOSOMAL PROTEINS.
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CYCLOHEXIMIDE, AN INHIBITOR OF
POLYPEPTIDE ELONGATION).
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PRESENTATION OF THE PRESEN
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ATPD_ECOLI
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Best Local S
Matches 7
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Hypothetical 18.4 kDa protein (ORF44).
Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nielsen J., Hansen F.G., Hoppe J., Friedl P., vor "The nucleotide sequence of the atp genes coding a, b, c and the F1 subunit delta of the membrane
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDITINE=85121806; PubMed=6395859;
Walker J.B., Gay N.J., Saraste M., Eberle A.N.;
"DNA sequence around the Escherichia coli unc og
the sequence of a 17 kilobase segment containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase delta chain (EC 3.6.3.14).
ATPH OR UNCH OR PAPE OR B3735 OR 25233 OR ECS4677.
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                                                                                                                                                                                                                                          "The atp operon: nucl
                                                                                                                                                                                                                                                                                                                                                                                                         glmS
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Virology 229:381-399(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleopolyhedrovirus.
                                                                         SEQUENCE FROM N.A.
MEDLINE=82147764; PubMed=6278247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
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                                                                                                                                                                                      for the membrane proteins, ATP-synthase.";
                                                                                                                                                                                                                                                                                            MEDLINE=82059437;
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                                                                                                                                                                                                               operon: nucleotide sequence of the promoter and the genes membrane proteins, and the delta subunit of Escherichia co
                                                                                                                                                                                                                                                                                                                                                                        phos.";
J. 224:799-815(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteobacteria;
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Conservative
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                                                                                                                                                                                                                                                                                            PubMed=6272190;
                                                                                                                                                           9:3919-3926(1981).
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0; Mismatches
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  von Meyenburg K.;
ing for the F0 subunits
ane bound ATP synthase
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ing asnA, oriC, unc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=0157:H7 / RIMD 0509952;
STRAIN=0157:H7 / RIMD 0509952;
Hayashi T., Makino K., Ohnshim M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnshim M., Kurokawa K., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBGNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBGNITS: ALPHA (3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBGNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97307253; PubMed=9164460;
MEDLINE=97307253; PubMed=9164460;
Wilkerns S., Duns S.D., Chandler J., Dahlquist F.W., Capaldi R.A.;
Wilkerns structure of the N-terminal domain of the delta subunit of
the E. coli ArPeynthase...;
Nat. Struct. Biol. 4:198-201(1997).
-!- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LINKS
CF(0) TO CF(1). IT EITHER THANSMITS CONFORMATIONAL CHANGES FROM
CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=93135143; PubMed=7686882;
Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
Burland V.D., Plunkett G. III, bakilobases of the Escherichia coli
Burland vequence and analysis of 136 kilobases of the Escherichia coli
genome: organizational symmetry around the origin of replication.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                             MEDLINE-82068433; PubMed-6458296; Mabuchi K., Kanazawa H., Kayano T., Futai M.; Machochi K., Kanazawa H., Kayano T., Futai M.; Mucleotide sequence of the gene coding for the delta subunit of proton translocating ATPase of Escherichia coli."; Biochem. Biophys. Res. Commun. 102:172-179(1981).
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=0157.H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                    . Gen. Genet. 184:33-39(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J01594; AAA24734.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                   Genomics 16:551-561(1993)
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Escherichia coli.";
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                                      PIR; A01031; PWECD.

PDB; 1ABV; 07-JUL-97.

ECGGEN; ECGGEN; B.

PRINTS; PRO10213; OSCP; 1.

PRINTS; PRO125; ATPAEDEUTA.

TIGREAMS; PRO1025; ATPAEDEUTA.

PROSITE; PRO1039; ATPAEDEUTA;

Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Dorsal root ganglion;
MEDLINE=99348269; Pubmed=10419452;
Jordan J.D., Carey K.D., Stork P.J.S., Iyengar R.;
"Modulation of Rap activity by direct interaction of Galphao with Rapl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTPASE-activating protein.";
J. Biol. Chem. 274:21507-21510 (1999).

ACTIVITY OF G PROTEIN ALPHA SUBUNITS THERBRY DRIVING THEM INTO THEIR INACTIVE GDP-BOUND FORM.

SUBCELLULAR LOCATION: Membrane-bound (Potential).

SUBCELLULAR LOCATION: Membrane-bound (Potential).

PTM: FATTY ACYLARED. HAVILY PALMITOYLATED IN THE CYSTEINE STRING MOTIF (BY SIMILARITY).
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Signal transduction inhibitor; Membrane; Lipoprotein; Palmitate.
DOMAIN 28
                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                     Length 177;
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6AFD9552A79C81A5 CRC64;
                                                                                                                                                                                                                                                    1.0%; Score 7; DB 1;
100.0%; Pred. No. 32;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  210 AA.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat.
Regulator of G-protein signaling 17 (RGS17)
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Pfam; PF00615; RGS; 1.
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ProDom; PD001580; Reg of prG; 1.
SMART; SM00315; RGS; 1.
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                                                                                                                                                                                                                        SEQUENCE 177 AA; 19332 MW;
EMBL; AE000450; AAC76758.1;
             AE005605; AAG58938.1;
AP002566; BAB38100.1;
                                                                                                                                                                                                                                                                                     7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken)
                                                                                                                                                                                        Complete proteome.
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RGSH_CHICK
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peeole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT "Functional and the second sec
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SEQUENCE
                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
-!- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=Olfactory bulb;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulator of G-protein signaling 17 (RGS17) (Regulator of Gz-selective protein signaling 2). RGS17 OR RGS22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QZB0;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
                                                                                                                                                                                                                                                                 THEIR INACTIVE GDP-BOUND FORM.
SUBCELLULAR LOCATION: Membrane-bound (Potential).
PTM: FATTY ACYLATED. HEAVILY PALMITOYLATED IN THE
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100.0%; Pred. No.
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6581AAD5BADDEE7C
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5. 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96172747; PubMed=8589412;
Roest H.P., Mulders I.H.M., Wijffelman C.A.,
"Isolation of ropB, a gene encoding a 22-kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium leguminosarum (biovar viciae).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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15-DEC-1998
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ProDom; PD001580; Reg_of_prG
                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                              Antigen; Outer membrane; Signal
                                                                                                                                                                                                                                                                                                                                      EMBL; X80767; CAA56751.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Outer membrane.-!- SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Plant Microbe Interact. 8:576-583(1995).
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                                                                                                                                                                                                                                                                                 Pfam; PF01389; OmpA_membrane; 1.
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.5-DEC-1998
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115
                                               209 GSVRGRV 215
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GSVRGRV 12:
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                                                                                            Conservative
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3S; 1.
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22 KDA OUTER MEMBRANE PROTEIN
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                                                                                                                                           DB 1;
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Rhizobium leguminosarum
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EMBL; AF191555; AAF05758.1; -.

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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00272; END; 2.
PROSITE; PS00270; ENDOTHELIN; 2.
Cleavage on pair of basic residues; Vasoconstrictor; Multigene family;
                                                                                                                                                                                                                                                                               Baynash A.G., Hosoda K., Giaid A., Richardson J.A., Emoto N., Hammer R.E., Yanagisawa M., "Interaction of endothelin-3 with endothelin-B receptor is essential for development of epidermal melanocytes and enteric neurons.";
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OMPW OR VCA0867.

Vibrio cholerae.

Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

NCBI_TaxID=666;
                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                              Cell 79:1277-1285(1994).
-!- FUNCTION: ENDOTHELINS ARE ENDOTHELIUM-DERIVED VASOCONSTRICTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE ENDOTHELIN/SARAFOTOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 214;
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ENDOTHELIN LIKE.
BY SIMILARITY.
BY SIMILARITY.
                                                              01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Endothelin-3 precursor (ET-3).
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01-AUG-1990 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Mismatches
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                 PRT;
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                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=95094302; PubMed=8001160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:95285; Edn3.
InterPro; IPR0019641; Endothelin.
InterPro; IPR001928; Endothlin_tox.
Pfam; PF00322; endothelin; 1.
PRINTS; PR00365; ENDOTHELIN.
ProDom; PD005286; Endothelin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.0%; Scc.
100.0%; Pre
                                                       (Rel. 33, Created)
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                 STANDARD;
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117
173
111
                                                                                                                                                 Mus musculus (Mouse).
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Best Local Similarity
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                                                       01-FEB-1996
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OMPW_VIBCH
             ET3 MOUSE
P48299;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-E1 Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Vamayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
[1]
SEQUENCE FROM N.A.
MEDLINE=90245674; PubMed=2336399;
Malajakumari M.B., Manning P.A.;
"Nucleotide sequence of the gene, ompW, encoding a 22kDa immunogenic outer membrane protein of Vibrio cholerae.";
Nucleic Acids Res. 18:2180-2180(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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100.0%; Pred. No. 38;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406:477-483(2000).
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: TO B.COLI OMPW AND P.OLEOVORANS ALKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISSING (IN REF. 1).

SS -> LA (IN REF. 1).

O -> H (IN REF. 1).

A -> N (IN REF. 1).

F -> N (IN REF. 1).

G -> S (IN REF. 1).

AG -> NA (IN REF. 1).

AG -> Y (IN REF. 1).

S -> Y (IN REF. 1).

M -> I (IN REF. 1).
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P39621;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spore coat polysaccharide biosynthesis protein spsA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Outer membrane; Antigen; Complete proteome
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RA Kunst F. Ogsaswara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braum M., Brignell S.C., Bron S.,
RA Borriss R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Hailo M.F., Itaya M., Jones L.,
RA Gliseppi G., Guy B.J., Haga K., Hallo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viaria A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Withers P., Wipat A., Yamanecto H., Yamane K., Yasumoto K., Yata K.,
Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus
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Kunst F., Cyc

Kunst V., P
EMBL; X73124; CAA51619.1; -.
EMBL; Z99123; CAB15817.1; -.
PDB; 1QG9; 21-APR-00.
PDB; 1QG9; 04-MAY-00.
PDB; 1QG9; 04-MAY-00.
SubtiList; BG10609; SPSA.
InterPro; 1PR001173; Glycos_transf_2; 1.
Pfam; PF00535; Glycos_transferase; 3D-structure; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charnock S.J., Davies G.J.;

"Structure of the nucleotide-diphospho-sugar transferase, Sg. Bacillus subtilis, in native and nucleotide-complexed forms. Biochemistry 38:6380-6385(1999).

-i- FUNCTION: GLYCOSYLTRANSFERASE IMPLICATED IN THE SYNTHESS
                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentites requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presecan E., Santana M., Schmeider E., Schweizer J., Vertes A., Rapoport G., Danchin A.; "Bacillus subtilis genome project: cloning and sequencing of the kb region from 325 degrees to 333 degrees."; Mol. Microbiol. 10:371-384(1993).
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Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.
Presecan E., Santana M., Schneider E., Schweizer J., Vertes A.,
                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99280694; PubMed=10350455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Spore coat
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COAT
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                                                                                                                                                                                                                                                                                                                                                                                                            polysaccharide biosynthesis.
TO THE GLYCOSYLTRANSFERASE FAMILY 2.
                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                           and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNTHESIS
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RESULT 24
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L. Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Hube Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                           SEQUENCE
                                                                                                                         NP_BIND 88
                                                                                                                                                                Pfam; PF00288; GHMP_kinases; 1.
TIGRFAMS; TIGR00154; ispE; 1.
                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the statement of the statement is not removed.
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 392:353-358(1998).
-!- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POS:
GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aeolicus
                                                                                                                                                  Transferase; Kinase; Isoprene biosynthesis; ATP-binding
                                                                                                                                                                                                                       EMBL; AE000713; AAC07027.1; -.
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InterPro; IPR004424; IspE.
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 152
                           586 VETEISG
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7; Conserv
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268 ‡
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256 AA;
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29788 MW;
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                                                                  Score 7; I
Pred. No.
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Pred. No.
                                                                                                                      ATP (POTENTIAL)
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                                                                                                           C905F9B988E0B45D CRC64;
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                                                    Mismatches
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(See http://www.isb-sib.ch/announce/
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                                                                              Length 268
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MEDLINE=97061201; PubMed=8905231;
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P14609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: INVOLVED IN POTASSIUM TELLURITE RESISTANCE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-95550630, PubMed=7542800;
Relatine-95550630, Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kellay J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geognagen N.S.M.,
Wenter J.C.,
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable nicotinate-nucleotide pyrophosphorylase (carboxylating)
(EC 2.4.2.19) (Quinolinate phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000051; SAM bind.
InterPro; IPR004537; TehB.
TIGRPAMB; TIGRO0477; tehB; 1.
Antibiotic resistance; Tellurium resistance; Complete proteome.
SEQUENCE 286 AA; 33019 MM; 69D7647E97CC74FA CRC64;
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Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
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Pred. No. 48;
0; Mismatches 0; Indels
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Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                               01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Trallurite resistance protein tehB homolog. TEHB OR HI1275.
                                                           286 AA
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Best Local Similarity
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SEQUENCE FROM N.A.
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NCBI_TaxID=727;
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                                                     TEHB HAEIN
P45134;
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P74301;
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RESULT 25
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                                                                                                                                                                                                                                                                                                                DNA Res. 3:109-136(1996).
-!- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate +
CO(2) = pyridine-2,3-dicarboxylate + 5-phospho-alpha-D-ribose 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elkins M.F., Earhart C.F.;
"Nuclocities sequence and regulation of the Escherichia coli gene for
"Intercolocitie ransport protein FepB.";
J. Bacteriol. 171:5443-5451(1989).
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.",

    diphosphare.
    PATHWAY: NAD biosynthesis, aspartate to NaMN; third (last) step.
    SIMILARITY: BELONGS TO THE NADC/MODD FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyridine nuclectide biosynthesis; Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 295 AA; 31973 MW; DBCF6F88362E0735 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ferrienterobactin-binding periplasmic protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Match 1.0%; Score 7; DB 1; Local Similarity 100.0%; Pred. No. 49; es 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 AA
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InterPro; IPR002638; QRPTase
Pfam; PF01729; QRPTase; 1.
Pfam; PF02749; QRPTase_N; 1.
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TIGREAMS; TIGR00078; nadC;
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Best Local S
Matches '7
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EMBL; X532...
PIR; JV0045; JV0045.
EcoGene; EG10294; fepB.
EnterPro; JPR002491; Peripla_BP.
Pfam; PF01497; Peripla_BP_2; 1.
Transport; Iron transport; Signal
Transport; 318
POTF
Transport; 318
PRC
                                                                     TRPD PASMU
P57856;
16-OCT-2001
16-OCT-2001
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stephens D.L., Choe M.D., Barhart C.F.;
"Escherichia coli periplasmic protein FepB binds ferrienterobactin.";
Microbiology 141:1647-1654(1995)
-i- FUNCTION: BINDS FERRIENTEROBACTIN; PART OF THE BINDING-PROTEIN-
DEPENDENT TRANSPORT SYSTEM FOR UPTAKE OF FERRIENTEROBACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-57 FROM N.A.

MEDLINE=90230305; PubMed=2139473;

Brickman T.J., Ozenberger B.A., McIntosh M.A.;

"Regulation of divergent transcription from the entC promoter-operator regions in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mau I
          Bacteria; Pr
Pasteurella.
                                              Anthranilate phosphoribosyltransferase TRPD OR PM0581.
                                                                                                                                       PASMU
                                                                                                                                                                                                                                                                                             SEQUENCE
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EMBL; U82598; AAB40791.1; --
EMBL; X53274; CAA37370.1; --
PIR; JV0045; JV0045.
EcoGene; EG10294; fepB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chung E., Allen E., Araujo R., Aparicio A., Davis K., Dunc Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lev Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M29730; AAA83853.1;
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mes '7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Periplasmic.
INDUCTION: CONTROLLED IN PART BY THE AMOUNT OF AVAILABLE IRON.
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
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nce 277:1453-1474(1997).
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                     Proteobacteria;
                                                                                                                                                                                                                                                                                             318
                                                    (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
(Rel. 41, Last annotation update)
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ilarity 100.0%;
Conservative
                                    multocida
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                                                                                                                                                                                                                                                                                             34283 MW;
                     gamma
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Signal; Periplasmic;
POTENTIAL.
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Pred. No. 53;
0; Mismatches
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                      subdivision;
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                      Pasteurellaceae;
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RESULT 29
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Matches
                                                                              Pleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkne Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merri McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J. Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brando Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H. Wenter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete
SEQUENCE
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SEQUENCE FRO
STRAIN=Pm70;
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"Complete genomic sequence of Pasteurella mulcocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).

-!- CATALYTIC ACTIVITY: Anthranilate + phosphoribosylpyrophosphate =

N-5'-phosphoribosyl-anthranilate + diphosphate.

-!- PATHMAY: Tryptophan biosynthesis; second step.

-!- SIMILARITY: BELONGS TO THE ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE
                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE006093; AAK02665.1;
InterPro; IPR000312; Glycos transf 3, 1.
Pfam; PF00591; Glycos transf 3; 1.
Pfam; PF02885; Glycos transf 3; 1.
ProDom; PD001864; Glycos transf 3; 1.
ProDom; PD005916; Thymid phosphis; 1.
TIGRFAM6; TIGR01245; trpD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                 HAEIN
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                          Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995
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32, Last sequence update)
41, Last annotation update)
"1ransferase, catabolic (EC
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degradation
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Pred. No
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                          phosphate
                                                                                  J.L., Geoghagen N.S.M.,
V., Fraser C.M., Smith H.O
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                                                                     assembly
arginine
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                            L-ornithine
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MEDLINE=21848401; PubMed=11859360;

Mood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squores U., Feat N., Hayles J., Basken D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Nibler K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Sanders R., Starp S.,

Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

Nocdward J., Volckaert G., Avalsk R., Warren T., Whitehead S.,

Woodward J., Volckaert G., Andler R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Bger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Andlibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Bager P., Zimmermann W., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

Baga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 7; DB 1; Length 334;
100.0%; Pred. No. 55;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                        e; Arginine metabolism; Complete proteome.
334 AA; 37647 MW; B44B9ED2C1BB57F5 CRC64;
            -i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomyctales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UND-2002 (Rel. 41, Last annotation update)
15-UND-2002 (Rel. 41, Last annotation update)
SPAC2267.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 AA
                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGR00658; orni_carb_tr; 1.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
SUBUNIT: HOMOTRIMER (BY SIMILARITY).
                                                                                                                                                                                                                            InterPro; IPR002029; Asp/Orn Cotranf.
InterPro; IPR002222; Orn carbtransf.
Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace, N. 1.
                                                                                                                                                                                EMBL; U32741; AAC22253.1; -. HSSP; P08308; 10RT.
                                                                                                                                                                                                                                                                                         PRINTS; PR00100; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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254 YQVTPEL 260
                                                                                                                                                                                                                TIGR; HI0596; -
                                                                                                                                                                                                                                                                                                                                         Transferase;
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Q09801;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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        Forsburg S.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spierings G., Ockhuigen C., Hofstra H., Tommassen J.;
Characterization of the Citrobacter freundii phoE gene and
Characterization of the Citrobacter freundii phoE gene and
evelopment of C. freundii-specific oligonuclectides.";
FEMS Microbiol. Lett. 78:199-204 (1992).
-!- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE
GROWN UNDER PHOSPHATE LIMITATION. ITS ROTEIN PORE IS
PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schlzosaccharomyces pombe.";
Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 344 AA; 37290 MW; 571D391D0F88F27D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.0%; Score 7; DB 1;
100.0%; Pred. No. 56;
tive 0; Mismatches
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15-DEC-1998 (Rel. 37, Last annotation update)
Outer membrane pore protein B precursor.
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InterPro; IPR001329; OMP.2.
InterPro; IPR001702; PorIn gram-ve.
Pfam; PP00267; Gram-ve_porIns; 1.
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                                                                                                                                                                                                  -!- SIMILARITY: TO YEAST FIPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z54328; CAA91134.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Citrobacter freundii.
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les 7; Conserv
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RESULT 32
MURB_TREPA
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Best Local Similarity
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Best Local S
Matches 7
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SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spirochete.";
Science 281:375-388(1998).
Science 281:375-388(1998).
-!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
-!- COPACTOR: FAD (BY SIMILARITY).
-!- CATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: BELONGS TO THE MURB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeodd M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last annotation update) UDP-N-acetylenolpyruvoylglucosamine reductase
                                                                                                                                Pfam; PF01565; FAD_binding_4; 1.
Pfam; PF02873; MurB_C; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Oxidoreductase;
NADP; Flavoprotein; FAD; Complete proteome.
SEQUENCE 354 AA; 38595 MW; 809E56E606F5BFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                   EMBL; AE001193; AAC65086.1; -. TIGR; TP0090; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hatch B., Hc
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MURB OR TP0090
                                                                                                                                                                                                                                         InterPro; IPR003170; MurB.
InterPro; IPR001575; Oxid_FAD_bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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15-DEC-1998
461 LSLIGGG 467
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7; Conserv
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(Rel. 37, Last sequence update)
(Rel. 41, Last annotation updat
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38807 MW;
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                                                          Mismatches
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Query Match
Best Local :
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01-FEB-1994
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P23164;
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Q03946;
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CONFLICT
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Shigella dysenteriae Plasmid Invasion.
                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD003462; ASFV 360; 1.
SMART; SM00248; ANK; 1.
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Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90219205; PubMed=2325203; MEDLINE=90219205; PubMed=2325203; MEDLINE=90219205 V., Almazan F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             African swine fever virus (strain BA71V) (ASFV)
Viruses; dsDNA viruses, no RNA stage; Asfarviri
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Rodriguez J.F., Vinuela E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10498;
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InterPro; IPR002595; ASFV_360.
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4841A8165647BFE3 CRC64;
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P05423;
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                                                                                                            Mol. Microbiol. 5:2217-2221(1991).
-!- FUNCTION: ASSOCIATED WITH THE ENTRY OF THE BACTERIA INTO COLONIC EPITHELIAL CELLS.
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BUDILINE=89657927; PubMed=31057506;
Venkatesan M.M., Buyses J.M., Kopecko D.J.;
"Characterization of invasion plasmid antigen genes (ipaBCD) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid 210 kb invasion pWR100, and Plasmid 230 kb pMYSH6000.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                            Yao R., Palchaudhuri S.;
"Nucleotide sequence of the ipaBCD structural genes of Shigella
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STRAIN=SERCYPPD 2A, PLASMID=230 kb pMYSH6000;
MEDLINE=90014179; PubMed=2552264;
Sasakawa C., Adler B., Tobe T., Okada N., Nagai S., Komatsu K.,
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100.0%; Pred. No. 62;
cive 0; Mismatches 0; Indels
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"Nucleotide sequence of the invasion plasmid antigen B
(ipaB and ipaC) of Shigella flexneri.";
Microb. Pathog. 4:345-357(1988).
                                                                                                                                                                                                                                                                                                           A22E1D6399EC90BF CRC64;
                                                                                                                                                                                                                                                                         Antigen; Plasmid; Virulence, Membrane, Signal.
SIGNAL 19 BY SIMILARITY.
CHAIN 20 382 42 KDA MEMBRANE ANTIGEN
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01-NOV-1990 (Rel. 16, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                 MEDLINE=92114800; PubMed=1766387;
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MEDLINE=89200844; PubMed=3071655;
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           Shigella.
NCBI_TaxID=622;
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P18012;
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"Isolation of the human gene that complements a temperature-sensitive
cell cycle mutation in BHK cells.";
Mol. Cell. Biol. 7:3386-3393(1987).
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                                                                                                                    PARTIAL SEQUENCE OF 20-64 AND 318-335.
MEDLINE-89307550; PubMed-2663721;
Sankaran K., Ramachandran V., Subrahmanyam Y.V.B.K., Rajarathnam S.,
                                                                                                                                                                                                                                                                                                   Infect. Immun. 57:2364-2371(1989).
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"Functional organization and nucleotide sequence of virulence Region-2 on the large virulence plasmid in Shigella flexneri 2a."; Mol. Microbiol. 3:1191-1201(1989).
                                                                                                                                                                                                                                                                                                                                                             EPITHELIAL CELLS.
-!- MISCELLANEOUS: SYNTHESIS OF THIS IMMUNOGEN IS REPRESSED AT 30 DEGREES CELSIUS AND RESTORED AT 37 DEGREES CELSIUS.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                             Elango S., Roy R.K.; "Congo red-mediated regulation of levels of Shigella flexneri 2a
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tive 0; Mismatches 0; Indels
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01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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BN51T OR BN51.
Homo sapiens (Human).
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MEDLINE=92295566; PubMed=1318606;
Telford E.A.R., Watson M.S., McBride
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                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                 Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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                                                                                                                                                                                                                                                         "The DNA sequence of equine herpesvirus-1.";
Virology 189:304-316(1992).
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TO THE C-TERMINUS OF YEAST RPC4.
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          (See http://www.isb-sib.
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RESULT 39
GLUP_BRUAB
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AC Q44623;
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P32514;
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                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                Kinkou M., Fukushi H., Matsumura T., Kim S.K., O'Callagh Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSVEK
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InterPro; IPR003363; Herpes_gG.
Pfam; PF02400; Herpes_gG; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Equine herpesvirus type 1 (strain Kentucky A)
Viruses; dsDNA viruses, no RNA stage; Herpesv:
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=10329;
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                                                                                                                                                        SEQUENCE
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SIGNAL
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15-JUN-2002
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                                                                 16 TVLAALS 22
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3 TVLAALS 9
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
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(See http://www.isb-sib.ch/announce/
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6 outstation -
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                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE FHS (TC 2.1.7) FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         Essenberg R.C., Candler C., Nida S.K.;
"Brucella abortus strain 2308 putative glucose and galactose
transporter gene: cloning and characterization.";
Microbiology 143:1549-1555(1997).
-: FUNCTION: INTAKE OF GLUCOSE AND GALACTOSE (FOTENTIAL).
-: SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 7; DB 1; Length 412;
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NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; U43785; AAB58958.1; -.
TIGRRAMs; TIGRO1272; glub; ll.
Sugar transport; Transmembrane; Inner membrane.
TRANSMEM 21 41 POTENTIAL.
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 39, Last annotation update)
Glucose/galactose transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TP0118.
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388 4
412 AA;
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                                                                                                                        SEQUENCE FROM N.A.
                                                           Brucella abortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 KALAFDA 370
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-!- CATALYTIC ACTIVITY: ATP + {tetrahydrofoly1-[Glu]}(N) + L-glutamate
= ADP + phosphate + {tetrahydrofoly1-[Glu]}(N+1).
-!- PATHWAY: BACTERIA REQUIRE FOLATE FOR THE BIOSYNTHESIS OF GLYCINE,
METHIONINE, FORMYL-MET-TRNA, THYMIDYLATES, PURINES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Harch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Folybolyglutamate synthase (EC 6.3.2.17) (Folylpoly-gamma-glutamate synthetase) (FPGS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=5550630, PubMed=7542800, Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Merrick J.M., Merrick J.M., Strichnon G., Fitzhugh W., Fields C.A., Gocayne J.D., Soutt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Witerback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 269:496-512(1995).
-!- FUNCTION: CONVERSION OF FOLATES TO POLYGLUTAMATE DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                      'Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein, Coiled coil, Complete proteome.
DOMAIN 126 182 COILED COIL (POTENTIAL).
DOMAIN 328 397 COILED COIL (POTENTIAL).
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0; Mismatches
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100.0%; Pred. No
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TIGR; TP0118; -.
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1 / KW20 / ATCC 51907;
                                                                                                                                                                     Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100...
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOLC OR HI1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Rd /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOLC HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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FOLC_HAEIN
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UVSH_EMENI STANDARD; PRT; 443 AA.

ID TUSH_EMENI STANDARD; PRT; 443 AA.

AC Q02398; Q00178;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Postreplication repair protein uvsH/nuvA.
GN UVSH OR NUVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ś
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HSSP; P15925;
TIGR; HI1261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001645; Fpolygl synthtse.
InterPro; IPR000713; Mur_ligase.
Pfam; PF01255; Mur_ligase; 1
PROSITE; PS01011; FOLYLPOLYGLU SYNT_1; 1.
PROSITE; PS01011; FOLYLPOLYGLU SYNT_2; 1.
PROSITE; PS01012; FOLYLPOLYGLU SYNT_2; 1.
Ligase; One-carbon metabolism; ATP-binding; Comp.
NP_BIND 55 61 ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
Mol.
                     use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                            This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinforthe European Bioinformatics Institute the European Bioinformatics Institute Instit
                                                                                                                                                                                                                                                                                                                                                                                                 Iwanejko I.A., Cotton C.M., Jones G.W., Tomsett A.B., Strike p. "nuvA, an Aspergillus nidulans gene involved in DNA repair and recombination, is a homologue of Saccharomyces cerevisiae RADII Neurospora crassa uvs-2."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF
STRAIN=L20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Aspergillus uvsH gene encodes a and Neurospora UVS-2.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eurotiales; Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                               Microbiology 142:505-515(1996).
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                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear (By similarity). SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                             FUNCTION: Involved in postreplication repair of Postreplication repair functions in gap-filling strand on replication of damaged DNA. Has ssDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora UVS-2
                                                                                       SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                          (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .H., Lee B.J.,
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non-profit institutions as long as its content
and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF 1-356 FROM N.A.
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437 AA;
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                                          oved. Usage by and fo
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of a daughter
binding activity
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tent is in
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RESULT
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Matches 7
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InterPro; IPR003034; SAP.
InterPro; IPR001841; Znf ring.
Pfam; PF00097; zf-C3HC4; 1.
Pfam; PF02037; SAP; 1.
SMART; SM00184; RING; 1.
SMART; SM00513; SAP; 1.
TIGRPAMS; TIGR00599; rad18; 1.
PROSITE; PS00518; ZF RING 1; 1.
PROSITE; PS00518; ZF RING 2; 1.
Zinc-finger; DNA-binding; DNA dam ZN FING 36 SAP.
CONFLICT 209 210 FG-CONFLICT 209 210 FG-
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- SR54 AQUAE
- O67615;
- 30-MAY-2000
- 30-MAY-2000
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
HSSP;
                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                       EMBL; AE000753;
HSSP; O07347; 11
                                                                                                                                                                                                                                                                                                             Deckert G., Warren P.V., Gaasterland T., Young W.G., Len
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal recognition FFH OR AQ_1720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
Signal recognition particle protein (Fifty-
                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                   aeolicus
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=VF5;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aquifex aeolicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 LIANARK 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 LIANARK 430
                                                                                                                                                               FUNCTION: BECESSARY FOR EFFICIENT EXPORT OF EXTRA-CYTOPLASMIC PROTEINS. BINDS TO THE SIGNAL SEQUENCE WHEN IT EMERGES FROM TRIBOSOMES (BY SIMILARITY).

SUBUNIT: SIGNAL RECOGNITION PARTICLE CONSISTS OF A 4.5 RNA MOLECULE AND PROTEIN FFH (BY SIMILARITY).

DOMAIN: THE PROTEIN HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE RNA AND ALSO BINDS THE SIGN SEQUENCE.

SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          $79392; AAB35098.1;
Z49875; CAA90033.1;
P15919; 1RMD.
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Conservative
                        1FFH
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                                    AAC07579.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Aquificae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.0%;
                                                                                                                                                                  TO THE SRP FAMILY OF GTP-BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA damage;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (class); Aquificales; Aquificaceae;
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DD3327065D3511B2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on update)
(Fifty-four
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                                                                                                  There are no rest
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                                                                                                                                                                                                                                                            EXTRA-CYTOPLASMIC IT EMERGES FROM THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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ay M., Huber
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                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elongation factor 1-alpha (EF-1-alpha) (50 kDa actin-binding protein)
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-TU/EF-1A SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elongation factor 1a.";
Nature 347:494-496(1990).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF AMINOACYL-TRNA TO THE A.SITE OF RIBOSOMES DURING PROTEIN BIOSYNTHESIS. IT IS ALSO AN ABUNDANT ACTIN FILAMENT BUNDLING
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang F., Demma M., Warren V., Dharmawardhane S., Condeelis J.; "Identification of an actin-binding protein from Dictyostelium
                                                                                                                                                                                                      1.0%; Score 7; DB 1; Length 454;
100.0%; Pred. No. 71;
ive 0; Mismatches 0; Indels
                                                                                                                        289 G-DOMAIN.
454 M-DONAIN.
109 GTP (BY SIMILARITY).
186 GTP (BY SIMILARITY).
245 GTP (BY SIMILARITY).
50911 MW, 9F13FA8C683A0558 CRC64;
        InterPro; IPR004780; SRP eub.
Pfam; PF00448; SRP54; 1.
Pfam; PF02978; SRP54; 1.
ProDom; PF002978; SRP54; 1.
ProDom; PF000819; SRP54; 1.
SNART; SM00382; AAA; 1.
TIGRFAM9; TIGR00599; 315051801; 1.
PROSITE; PS00300; SRP54; 1.
Signal recognition particle; GTP-binding; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44669;
                                                                                                                                                                                                                                                                                                                                  456 AA
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MEDLINE=91015340; PubMed=2215665;
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DictyDb; DD01027; efaA.
InterPro; IPR004539; EFTJ alpha.
InterPro; IPR004160; EFTJ Cterm.
InterPro; IPR004161; EFTJ D2.
InterPro; IPR004161; EFTJ D2.
  InterPro; IPR004125; SRP54_SPB
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NCBI_TaxID=2787;
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF01143; GTP_EFTU_D2; 1.
PFAM; PF01144; GTP_EFTU_D2; 1.
PR03144; GTP_EFTU_D2; 1.
TIGREAM: PR00315; ELONGATNFCT.
TIGREAM: TIGR00483; EF-1 alpha; 1.
PR051TF; PS00301; EFACTOR_GTP; 1.
PR051TF; PS00301; EFACTOR_GTP; 1.
PR051TF; PS00301; EFACTOR_GTP; 1.
NP_BIND 17 24 GTP (BY SIMILARITY).
NP_BIND 156 159 GTP (BY SIMILARITY).
SEQUENCE 456 AA; 50066 MW; BCFE9E1B70C3D8A8 CRC64;
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Submitted (Nov-1995) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES. IT

BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BETA

-:- CHAIN AND ONE AT A NOWEKTHANGEABLE SITE ON THE ALPHA-CHAIN.

-!- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.

-!- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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INGETPO; IPRO02453; Beta_tubulin.
InterPro; IPRO00217; Tubulin.
InterPro; IPRO03008; Tubulin. Ft82.
Ft8n; PPO0091; tubulin; 1.
PROSITE; PS00227; TUBULIN; 1.
PROSITE; PS00228; TUBULIN; MILLIGENE family.
NP BIND 140 146
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tive 0; Mismatches
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Patent No. 5882851

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APPLICANT: Moller, Birger L.
TITLE OF INVENTION: Cytochrome P-450 Monooxygenases

NUMBER OF SEQUENCES: 24

CORRESPONDENCE 3. 24

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ZIP: 27709

COMPUTER: READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Darber PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,177A
FILING DATE: 08-AUG-1996
CLASSIFICATION: 800
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TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 3:
CREMENTER SEQ ID NO: 3:
CREMENTER SECONDORSEY
US-09-196-293-6
US-08-602-999A-88
US-08-602-999A-89
US-08-602-999A-89
US-08-209-6018-6
US-08-278-865-90
US-08-278-865-90
US-09-500-124-89
PCT-US93-12246-4
PCT-US93-12246-4
PCT-US95-011495-2
PCT-US96-11495-2
US-08-642-255-103
US-08-469-569-126
US-08-469-568-126
US-08-377-598-126
US-08-377-598-126
US-08-377-598-126
US-08-469-568-126
US-08-377-598-126
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: 3054 Cornwallis Road
Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tree.
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Res
STATE: NC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-08-656-177A-3
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                                                                                                                                                                                                                     US-09-256-797-3

Sequence 3. Application US/09256797

Patent NO. 6133417

GENERAL INFORMATION:

APPLICANT: Koch, Birgit M.
APPLICANT: Koch, Birgit M.
APPLICANT: Bibbeson, Ole

APPLICANT: Halkier, Barbara Ann
APPLICANT: Moller, Birger L.

TITLE OF INVENTION: Cytochrome P-450 Moncoxygenases

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 6133417artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
                                                                                      0; Indels
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           Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/656,177
FILING DATE: 08-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 8-19783/A/PCT
TELECOMMUNICATION INFORMATION:
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERSISTICS:
LEGETH: AND ADD NO: 3:
LEGETH: ADD NO: 3:
LEGETH
   1.0%; Score 7; DB 2
100.0%; Pred. No. 7.1
ive 0; Mismatches
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100.0%; Pred. No. 7.1
tive 0; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 97, Application US/08817811; Patent No. 6174528
GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-09-256-797-3
Query Match
Best Local Similarity 100.1
Matches 7; Conservative
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Best Local Similarity 100.
Loca 7; Conservative
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US-08-817-811-97
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Query Match
Best Local Similarity
Thehes 7; Conserv
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INFORMATION FOR SEQ ID NO:
                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 75 amino acids
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PRIOR APPLICATION DATA:
APPLICATION UNDER: WO 96/11944

PILING DATE: 25-APR-1996

PILING DATE: 1996

PILIN
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILLING DATE: 14-APR-1997
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES TITLE OF INVENTION: COMPRISING SAME NUMBER OF SEQUENCES: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Relf, Wendy A.
APPLICANT: Good, Michael
APPLICANT: Saul, Allan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 512/418-3000
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TOPOLOGY: li
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STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 57,642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                                                                                                                                                                                                                                                                                               STREET:
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ZIP: 77210
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                    CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE:
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                                                                                                                                                                                                                                                                 Texas
                                                                                                                                                                                                                                                                                                                                   B: Arnold, White & Durkee
P.O. Box 4433
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                                                                                                                                                                                                                          USA
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Saul, Allan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Relf, Wendy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cooper, Juan A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0%; Score 7; DB .
100.0%; Pred. No. 26
ive 0; Mismatches
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Query Match
Best Local Similarity
Thes 7; Conserve
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US-08-817-811-20
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Patent No. 6
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INFORMATION FOR SEQ ID NO:
             TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
PILLING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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APPLICATION NUMBER: US
FILING DATE: 14-APR-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES TITLE OF INVENTION: COMPRISING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 ARGGLAL 413
                                                                                         NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FE
                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 ARGGLAL 29
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0, Application US/08817811
6174528
                                                                                                                                                                                                                                                                                                                                                                                                              Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                               Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                E: Arnold, Wh
P.O. Box 4433
78 amino acids
                                                512/474-7577
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Good, Michael F.
Saul, Allan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                               512/418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Juan A.
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                                                                                                            37,642
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ER: FBRC:005
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                                                                                                FBRC: 005
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5. 27;
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; TOPOLOGY: linear
US-08-817-811-19
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                                                                                                                                                                            MESULT 6
US-08-817-811-96
Sequence 96, Application US/08817811
Fatent No. 617428
GENERAL INFORMATION:
APPLICANT: Cooper, Juan A.
APPLICANT: Relf, Wendy A.
TITLE OF INVENTION: SYNTHETIC PEPTIDES
TITLE OF INVENTION: COMPRISING SAME
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
                                                                          1.0%; Score 7; DB 4; Length 78;
100.0%; Pred. No. 27;
ive 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,811
FILING DATE: 14-APR-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: FBRC:005
TELECOMMUNICATION NUMBER: FBRC:005
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: 512/418-3000
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o. 27;
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100.0%; Pred. No. 27;
cive 0; Mismatches
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Patent No. 6174528
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 7; Conservative
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; TOPOLOGY: li
US-08-817-811-20
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APPLICANT: GOOD, MICHAEL PRILATE OF PURPLICANT: SHILA ALL BO TUNEWRICHS: STATE OF PURPLICANT: SHILA ALL BO TUNEWRICHS: STATE OF PURPLICANT ON THE OF P
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US-08-817-811-95
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                                                                 REFERENCE/DOCKET NUMBER: FJI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 39:
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                          SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ODA, TOSHIO
TITLE OF INVENTION: THEREOF
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LENGTH: 79 amino acide
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REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: FBRC:005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 96/11944
FILING DATE: 25-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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nes 7; Conservative (
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STRANDEDNESS:
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ER: FJ
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                                                                                                                                                                                                                                                                                     Version #1.25
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o. 28;
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                                                              ; LOCATION: 1.127
; OTHER INFORMATION:
US-09-330-945-39
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Best Local Similarity 100.
"---hes 7; Conservative
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                                 Query Match
                                                                                                                                                                                                                   TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: FJ
                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/119,995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                               FEATURE:
                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA ENCODI
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y Match 1.0%; Score 7; DB 3; Local Similarity 100.0%; Pred. No. 42; hes 7; Conservative 0; Mismatches
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OTHER INFORMATION: /note= "XLN A SEQUENCE (FIGURE 4)"
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                                                                                                           NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/330,945
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6077946
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STON
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SEKI, NORIAKI
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100.0%; Pred. No.
ative 0; Mismatcl
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AMEBOCYTE LYSATE FACTOR G SUBUNIT
                                                                               /note= "XLN A SEQUENCE (FIGURE 4)"
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                               Length 127;
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                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08279996
| Patent No. 5552140
| GENERAL INFORMATION:
| APPLICANT: Boston, Rebecca S. APPLICANT: Bass, Henry W. APPLICANT: O'Brian, Gregory R. TITLE OF INVENTION: DNA Encoding A Ribosome Inactivating TITLE OF INVENTION: Protein
| NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESSE: CORRESPONDENCE ADDRESSE: ABDRESSE: Gibson ADDRESSEE: Gibson Sibley; Bell, Seltzer, Park and ADDRESSEE: Gibson Sibley; Bell, Seltzer, Park Statut Sta
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                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5552140th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279,996
FLING DATE: 05-JUL-1994
CLASSIFICATION NUMBER: US 07/941,651
FILING DATE: 08-SEP-192
ATFORNEY/AGENT INPOMMATION:
NAME: Sibley, Kenneth D.
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
                                              .
0
                Pred. No. 83;
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100.0%; Pred. ...
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US-08-746-797-2
; Sequence 2, Application US/08746797
; Patent No. 5759832
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel
; APPLICANT: Lonsdale, John
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 5651
TELECOMMUNICATION INFORMATION:
TELERAX: 919-881-3176
TELEX: 575102
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.0%; Soc
Best Local Similarity 100.0%; Pi
Matches 7; Conservative 0;
             Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                          558 KDKNAAA 564
                                                                                                                                                                     262 KDKNAAA 268
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US-08-279-996-2
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| Sequence 2, Application US/07941651
| Sequence 2, Application US/07941651
| Patent No. 5332808
| Patent No. 5332808
| APPLICANT: Boston, Rebecca S. APPLICANT: Bass, Henry W. TITLE OF INVENTION: DNA Encoding A Ribosome Inactivating TITLE OF INVENTION: DNA Encoding A Ribosome Inactivating TITLE OF INVENTION: Protein | NUMBER OF SEQUENCES: 6 CORRESPONDENCES: 6 CORRESPONDENCES: 6 CORRESPONDENCES: 6 ADDRESSEE Gibson STREET: Post Office Drawer 34009
| STREET: Post Office Drawer 34009 | STATE: No. 5332808th Carolina | STATE: No. 532808th Carolina | COUNTRY: U.S.A.
                                                                                                                                                                               ESSUD. 1.
5182262-8
; Pacent No. 5182262
; Pacent No. THOWAS
; TITLE OF INVENTION: CALMODULIN BINDING PEPTIDE DERIVATIVES
; OF NON-EXPINOID APPLICATION DATE:
; CURRENT APPLICATION DATE:
; APPLICATION DATE:
; APPLICATION DATE:
; FILING DATE: 02-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CLASSIFICATION NUMBER: 31,665
REGISTRATION NUMBER: 31,665
REBERENCE/DOCKET NUMBER: 5051-199
TELEPHONE: 919-881-3175
TELEPHONE: 919-881-3175
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. 75;
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Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 278 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
, MOLECULE TYPE: protein
US-07-941-651-2
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                205 LNSDGSV 211
                                                           LNSDGSV 89
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TELEX: 5'
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Length 278;

DB 1;

1.0%; Score 7;

Query Match

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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-746-797-2
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APPLICANT: Gentry
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SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acid
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APPLICATION NUMBER: No. 5759832 Yet Assigned FILING DATE: 23-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: N
ANTI-SENSE: NO
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                       COUNTRY:
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TLE OF INVENTION: NOVEL F
                                                                                                                                             19406-0939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Payne, David
                                                                                                                                                                              U.S.A.
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HYPOTHETICAL: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-termina
CRIGINAL SOURCE:
US-08-927-387-2
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Matches
                                                                 SUFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,058
FILING DATE: 25-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/746,797
FILING DATE:
ATTORNEW / 5-CTM:
ATTORNEW / 5-CTM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
              ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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FILING DATE: 23-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pearson, Stewart
TITLE OF INVENTION: NOVEL FabH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 SLNSDGS 184
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 SLNSDGS 210
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                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version
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                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                      TRY: U.S.A.
19406-0939
                                                                                                                                                                                                                                                                                                                                      King of Prussia
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Payne, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gentry, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ Version 1.5
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100.0%; Pr
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%; Pred. No. 95;
0; Mismatches
              PS0573
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Gaps

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RESULT 18

US-08-338-530A-3

i Sequence 3, Application US/08338530A

i Patent No. 592237

GENERAL INFORMATION:

APPLICANT: CRABB, Brendan S.

ADDRESSEE: 101ev & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STREET: 3000 K Street, N.W., Suite 500

STREET: 3000 K Street, N.W., Suite 500

CONDUTR: USA

ZIP: 20007-5109

COMPUTER: LIMP PC Compatible

COMPUTER: IMP PC Compatible

COMPUTER: IMP PC Compatible

COMPUTER: IMP PC Compatible

COMPUTER: IMP PC Compatible

OPERATING STEER: 25-0AN-1995

CURRENT APPLICATION DATA:

APPLICATION NUMBER: WO PCT/AU93/00253

FILING DATE: 28-MAY-1993

ATTORNEY AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40268/120/CSMB

TELEPHONE: (202)672-5399

FELENCOMMUNICATION INFORMATION:

TELEPHONE: COMPATION:

TELEPHONE: COMPATION:

TELEPHONE: COMPATION:

TELEPHONE: COMPATION:

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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0; Indels
                             Indels
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Sequence 3, Application US/09267384

Patent No. 613944

GENERAL INFORMATION:

APPLICANT: CRABB, Brendan S.

APPLICANT: CRABB, Michael J.

TITLE OF INTENTION: EQUINE HERPESVIRUS GLYCOPROTEINS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESSE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500
Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 7; Conservative
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TOPOLOGY:
US-08-338-530A-3
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Satisfacture No. 603071

GENERAL INFORMATION:
APPLICANT: KHUDYAKOV, YURI E.
APPLICANT: FIELDS, HOWARD A.
TITLE OF INVENTION: MOSAIC PROTEIN AND RESTRICTION
TITLE OF INVENTION: ENDONUCLEASE ASSISTED LIGATION METHOD FOR MAKING THE SAME NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: JONES & ASKEW, ILP
STREET: 191 Peachtree Street, N.W., 37th Floor
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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CURRENT APPLICATION DATA:
PLECATION NUMBER: US/08/921,887
FILING DATE:
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100.0%; Pred. No.
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ATTORNEY/AGENT INFORMATION:
NAME: WARREN, WILLIAM L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 03063-0380
TELEFAN: 404-818-3700
TELEFAX: 404-818-3700
TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 3030-1769
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                           INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: single
  610-270-4478
                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 7; Conservative
                       TELEFAX: 610-270-5090
TELEX:
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                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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  TELEPHONE:
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Gaps

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Length 352;

DB 3;

Score 7;

1.0%;

Query Match

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FILE REFERENCE: 53679

CURRENT PILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 74

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 64

LENGTH: 461

TYPE: PRT

ORGANISM: Arabidopsis thaliana
US-09-457-0468-64
               RESULT 21
US-08-468-812-8
                                                                                                                                 Query Match
Best Local Similarity
Watches 7; Conserve
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Sequence 8, Application US/08468812
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 64, Application US/09457046B Patent No. 6287835
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40268/120/CSMB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/338,530
FILING DATE: 25-JAN-1995
APPLICATION NUMBER: WO PCT/AU93/00253
FILING DATE: 28-MAY-1993
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                   277
                                                                                                       668 TFDAMAA 674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/267,384 FILING DATE: CLASSIFICATION:
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                                                                              TEDAMAA 283
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                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                           100.0%; PI
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                                                                                                                                                             1.0%; Score 7; DB 4; Length 461; 00.0%; Pred. No. 1.3e+02;
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GENERAL INFORMATION:

APPLICANT:

M neyr

Arja

APPLICANT: APPLICANT: APPLICANT:

Vehmaanper , Jari Fagerstr m, Richard Lantto, Raija

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US-08-590-563-8
                                                    RESULT 22
                                                                                                                                                                                                                                                US-08-468-812-8
Sequence 8, Application US/08590563 Patent No. 6300114
                                                                                                                                                                          Matches
                                                                                                                                                                                          Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/332,412
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 491 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bugaisky, Larry B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 1050.0340002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide POSITION IN GENOME: CHROMOSOME/SEGMENT: M64551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Actinomadura Xylanase Sequences and Methods TITLE OF INVENTION: of Use NUMBER OF SEQUENCES: 25
                                                                                                       447 LNSDGSV 453
                                                                                                                                       205 LNSDGSV 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/468,812 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                          Local Similarity 100.0%;
nes 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                          202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paloheimo, Marja
Suominen, Pirkko
Lahtinen, Tarja
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                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                 not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Richard
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                                                                                                                                                                           Score 7; DB; Pred. No. 1. 0; Mismatches
                                                                                                                                                                          1.4e+02;
                                                                                                                                                                                                        Length 491;
                                                                                                                                                                           Indels
                                                                                                                                                                           0
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Gaps

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GENERAL INFORMATION:
APPLICANT: Lynn Dougette-Stamm et al
APPLICANT: Lynn Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
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; OTHER INFORMATION: Description of Artificial Sequence: HAP4
US-09-319-989-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.0%; Score 7; DB 4; Length 557;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.0%; Score 7; DB 4; Length 554; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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Patent No. 588281A
Patent No. 588281A
Patent No. 588281A
PAPLICANT: Stabesen, Ole
APPLICANT: Halkier, Barbara Ann
APPLICANT: Moller, Birger L.
TITLE OF INVENTION: Cytochrome P-450 Monooxygenages
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
CURRENT FILING DATE: 1999-06-14

BARLIER APPLICATION NUMBER: PCT/NL97/00688

BEARLIER PILING DATE: 1997-12-12

BARLIER FILING DATE: 1996-12-12

BARLIER FILING DATE: 1996-12-12

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 554

TYPE: RPT

ORGANISM: Artificial Sequence
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5569, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 YDLNDNN 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 YDLNDNN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 KNGDYSS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 KNGDYSS 50
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LENGTH: 557
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US-08-656-177A-2
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Patent No. 6190914
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Grivell, Leslie A.
APPLICANT: Teixeira De Mattos, Maarten J.
APPLICANT: Teixeira De Mattos, Maarten J.
APPLICANT: Blom, Jolanda
TITLE OF INVENTION: METHODS FOR MODULATING METABOLIC PATHWAYS OF
TITLE OF INVENTION: METHODS
FILE FILE SETERENCE: 24615-22012.00
CURRENT APPLICATION NUMBER: US/09/319,989
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  APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
APPLICANT: Lahtinen, Tarja
TITLE OF INVENTION: Production and Secretion of Proteins of
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSE: STERENE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N.W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 7; DB 4; Length 491;
Pred. No. 1.4e+02;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/590,563
FILING DATE: 26-JAN-1996
CLASSIFICATION: S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/468,812
FILING DATE: 06-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR APPLICATION NUMBER: US 08/282,001
FILING DATE: 31-OCT-1994
CLASSIFICATION NUMBER: US 08/282,001
FILING DATE: 29-JUL-1994
CLASSIFICATION NUMBER: 33,086
REFERENCE DOCKET NUMBER: 1550.0340003
TELECOMMUNICATION: INFORMATION:
NAME: BUGALSKY LAWTENCE B.
REFERENCE DOCKET NUMBER: 15050.0340003
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 7; Conservative
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STRANDEDNESS: not
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US-09-256-797-2
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FILING DATE: 08-AUG-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19783/A/POTELECOMMUNICATION INFORMATION:
           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/656,17:

PRICATION NUMBER: 08-806-19-6

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/256,797
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sibbésen, Öle
APPLICANT: Halkier, Barbara Ann
APPLICANT: Moller, Birger L.
TITLE OF INVENTION: Cytochrome P-450 Monooxygenases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: P-450-Tyr
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                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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nes 7; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocial
                                                                                                                                                                                                                                                                                                                             STREET: 3054 COLUMNATION CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                         COUNTRY: U
REFERENCE/DOCKET NUMBER: S-19783/A/PCT
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                E: No. 6133417artis Corporation 3054 Cornwallis Road
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                                                                                                                                                                                                                                                                                                            USA
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100.0%; Pred. No. 1.
tive 0; Mismatches
                                                                                       08/656,177
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o. 1.5e+02;
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RESULT 28
US-09-347-878-16
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                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 240
                                                                                                               Sequence 16, Application US/09347878C Patent No. 6376210
                                                                                                                                                                                                                                                                           Matches
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APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-1
NUMBER OF SEQ ID NOS: 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes FILE REFERENCE: 2318-258 CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 661
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CLONE: P=450-Tyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                        478 EGKTLHK 484
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                                                                                                                                                                                                                                                                        Local Similarity 100.0%; es 7; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rommens, Johanna M. Myriad Genetics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simard, Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tavtigian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09564805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
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                                                                                                                                                                                                                                                                                                           1.0%;
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                                                                                                                                                                                                                                                                                         Score 7; 1; Pred. No.
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; Pred. No
                                                                                                                                                                                                                                                                           0
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o. 1.8e+02;
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o. 1.5e
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                                                                                                                                                                                                                                                                                                       Length 661;
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NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59283810 No. 5928381disk of No. 5928381th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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APPLICANT: Marcher, Dorthe
APPLICANT: Pedersen, Hanne H.
APPLICANT: Predersen, Thomas E.
APPLICANT: Nilsson, Thomas E.
TITLE OF INVENTION: A Combined Desizing and Bleaching
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: mouse
TISSUE TYPE: brain
FUBLICATION INFORMATION:
AUTHORS: Masayoshi Mishina
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 to 1239
US-08-026-139E-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
1.0%; Score 7; DB 1; Le
Best Local Similarity 100.0%; Pred, No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 0;
                APPLICATION NUMBER: JP 173155/1992
PILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
PILING DATE: 13-NOV-1992
APPLICATION NUMBER: JP 303878/1992
PILING DATE: 13-NOV-1992
ATORNEY/AGENT INFORMATION:
NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 22,389
REGISTRATION NUMBER: P-4551
TELEPHONE: (212) 986-2340
TELEPHONE: (212) 983-7733
INFORMATION FOR SEO ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/08687399
Patent No. 5928381
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NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4127
TELECOMMUNICATION: TELECOMMUNICATION:
TELECHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: Bingle strand
TOPOLOGY: linear
   26-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
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CLASSIFICATION: 008
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US-08-687-399-7
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US-09-405-728-2
IS-Quence 2, Application US/09405728
| Sequence 2, Application US/09405728
| Patent No. 6391316
| GENERAL INFORMATION:
| APPLICANT: Rioux, Clement | APPLICANT: SCHIVVERS | AND EXPRESSION OF HAEMOPHILUS SOMNUS | TILLE OF INVENTION: CLONING AND EXPRESSION OF HAEMOPHILUS SOMNUS | TILLE REPERENCE: 9000-0049.20 | CURRENT APPLICATION NUMBER: US/09/405,728 | CURRENT PILLING DATE: 1999-09-24 | EARLIER PILLING DATE: 1999-09-24 | EARLIER FILLING DATE: 1999-03-10 | NUMBER OF SEQ ID NOS: 5 | COURT | COU
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Patent No. 5502166
GENERAL INFORMATION:
ABABDATION:
ABABDATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Nishiohata Residence 1-107
STREET: 5214, Nishiohata Rachi
CITY: Niigata-shi
STRYE: Niigata-ken
                                                                                                                                                                                                                      1.0%; Score 7; DB 4; Length 714; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.0%; Score 7; DB 4; Length 971; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS v.5
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/026,138E
FILING DATE: 26-PEB-1993
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APPLICATION NUMBER: JP 39563/1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 971
TYPE: PRT
CRGANISM: Haemophilus somnus
US-09-405-728-2
SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 16
                                                                                                                                                                                              Query Match
Best Local Similarity 100...
7; Conservative
                                                                                             TYPE: PRT
CORGANISM: Homo sapiens
US-09-347-878-16
                                                                                                                                                                                                                                                                                                                                                            473 KIESGEG 479
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ZIP: 951
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US-08-026-138E-3
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; Sequence 4, Application US/08462467B
Patent No. 6210899
; GENERAL INFORMATION:
APPLICANT: Rosenbaum, Jan S
; ATTILE OF INVENTION: The Use of a BM
TITLE OF INVENTION: Complex for Sc:
TITLE OF INVENTION: Co-Transfected
TITLE OF INVENTION: BMP Receptor
                                                                                                                                                                                                                                                              US-08-462-467B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Sorangium cellulosum US-09-413-814-46
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US-08-687-399-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Bloecker, Petra
APPLICANT: Cino, Paul M
APPLICANT: Cougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46, Application US/09413814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198
EARLIER APPLICATION NUMBER: DE 198
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                        NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                                                                 673 RGRVMAQ 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 7; Conserv
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                        ADDRESSEE:
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E: The Procter & Gamble Company
11810 East Miami River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1385 amino acids
                                                                                            Rosenbaum, Jan S
VENTION: The Use of a BMP Protein Receptor
VENTION: Complex for Screening Bone Metabolism Actives and Cells
VENTION: Co-Transfected With a Type II BMP Receptor and a Type I
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.0%; Score 7; DB 4; Le
100.0%; Pred. No. 3.8e+02;
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No. 3.4e+02;
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Matches
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Patent No. 6210899
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (513) 627-0260 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                 ATTORNEY/AGENT INFORMATION:
NAME: HEYBKO, BART S.
REGISTRATION NUMBER: 32,572
REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                  COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,572
REFERENCE/DOCKET NUMBER: 54
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-0633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosenbaum, Jan S
TITLE OF INVENTION: The Use of a BMP Protein Receptor
TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells
TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor and a Type I
TITLE OF INVENTION: BMP Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580 LYARGGL 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 LYARGGL 411
                                                                                                                                                                                                                                                                                                                                                           CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: no
TOPOLOGY: not re
               TELEPHONE: (513) 627-0633
TELEFAX: (513) 627-0260
                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                      APPLICATION NUMBER: US/08/462,467B
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                                                                                                                                                                                                                                                                                                                                                     : Ross
E: OH
                                                                                                                                                                                                                                                                                                                        45061
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Hersko, Bart S.
32,572
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                                                                                                                                                                                                                                                                                                                                                                                               E: The Procter & Gamble Company
11810 East Miami River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1618 amino acids
                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                 435
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100.0%; Pred. No. 3.
tive 0; Mismatches
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o. 3.9e+02;
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INFORMATION FOR SEQ 1D NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
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Matches 6, Conserv
  BENERAL INFORMATION:
                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                   CITY:
STATE:
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Patent No. 6210899

GENERAL INFORMATION:

APPLICANT: Rosenbaum, Jan S

TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells TITLE OF INVENTION: Complex for Screening Bone Metabolism Actives and Cells TITLE OF INVENTION: Co-Transfected With a Type II BMP Receptor and a Type I TITLE OF INVENTION: BMP Receptor

TITLE OF INVENTION: BMP Receptor

NUMBER OF SEQUENCES: 39

CORRESPONDENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Procter & Gamble Company
STREET: 11810 East Miami River Road
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100.0%; Pred. No. 6.6e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                        Query Match 1.0%; Score 7; DB 4; Length 2887; Best Local Similarity 100.0%; Pred. No. 6.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Plan PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,467B
FILING DATE:
CLASSIFICATION NUMBER: 32,572
ATORNEY/AGENT INFORMATION:
NAME: HEFRENCE/DOCKET NUMBER: 5474R
TELEPHONE: (513) 627-0260
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 amino acids
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US-08-159-339A-836
; Sequence 836, Application US/08159339A
; Patent No. 6037135
                                             ; TOPOLOGY: not relevant ; MOLECULE TYPE: protein US-08-462-467B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: not relevant MOLECULE TYPE: protein 1-462-4678-8
SEQUENCE CHARACTERISTICS:
LENGTH: 2887 amino acids
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Matches 7; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                       TYPE: amino acid STRANDEDNESS: not
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US-08-462-467B-8
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### APPLICANT: Grey, Howard N.
### APPLICANT: Galls Series Alexandro
### APPLICANT: Collar Series Alexandro
### APPLICANT: APPLICANT SERIES A.
### APPLICANT: IN GALLS A.
### COMPUTER SERIES CONTINUED.
### APPLICANT SERIES A.
### APPLICANT NUMBER: US 00/129, 136
### APPLICANT ON SERIES A.
### APPLICANT NUMBER: US 00/129, 136
### APPLICANT ON SERIES A.
### APPLICANT NUMBER: US 00/129, 136
### APPLICANT ON SERIES A.
### APPLICANT NUMBER: US 00/129, 136
### APPLICANT ON SERIES A.
### APPLICANT ON SERI
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RESULT 38
US-08-191-866D-64
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MOLECULE TYPE: peptide
US-08-159-339A-891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,866D
FILING DATE: 4 February 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 64, Application US/08191866D
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APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5783195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus S-IBR-052 And Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cochran, Mark D
APPLICANT: Macdonald, Richard D.
                                                                                                                                                                                                             STATE: New York
COUNTRY: USA
ZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 RGPSGL 159
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                 CITY: New York
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100.0%; Pred. No. 45;
tive 0; Mismatches
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RESULT 40 PCT-US93-07306-45

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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-185-949B-64
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                              Query Match
Best Local Similarity 100.
Conservative
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Patent No. 5874279
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                                                                                                                                                                                             TELEFAX: (212) 278-05
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mark D. Coc
APPLICANT: Richard D.
TITLE OF INVENTION: Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                        472 YKIESG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           472 YKIESG 477
                                                                                                                                                     TYPE:
                                                                                                                                                                                                                                                  NAME: White, John P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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2 YKIESG 7
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New York
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OGY: linear
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                                                                                                                                                                                                            (212)
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                                                   100.0%; Pative 0;
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100.0%; Pred. No. 73
ive 0; Mismatches
                                                                                0.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macdonald
                                                                                                                                                                                                                                                     , 678
                                                                                                                                                                                             64:
                                                   Score 6; DB :; Pred. No. 73
0; Mismatches
                                                               DB 2;
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5. 73;
                                                                               Length 17;
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                                                    0; Indels
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GENGRAL INFORMATION:

APPLICANT: WGGeer, Patrick L.
APPLICANT: WGGeer, Patrick L.
APPLICANT: Rothenberger, Sylvia
APPLICANT: Rothenberger, Sylvia
APPLICANT: Rothenberger, Sylvia
APPLICANT: Rothenberger, Sylvia
APPLICANT: Wennard, Malcolm
APPLICANT: Wennard, Malcolm
TITLE OF INVENTION: use of ps7 and Iron Binding Proteins
TITLE OF INVENTION: use of ps7 and Therapeutic Agents
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereskin & Parr
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3YZ
COMPUTER: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
COMPUTER: Date Compatible
OPERATIOG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: us/09/285,040
FILIGO DATE: 01-APR-1999
CLASSIFICATION: UNDRER: 40,261
REFERENCE/DOCKET NUMBER: 7685-032
TELECOMMUNICATION INDREMATION:
NAME: Gravelle, Micheline
REFERENCE/DOCKET NUMBER: 7685-032
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
TELECOMMUNICATION INDREMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,933
FILING DATE: August 31, 1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Shona S: McDiarmid
REGISTRATION NUMBER: 38,798
RESTRENCE/DOCKET NUMBER: 7685-006
TELECOMMUNICATION INFORMATION:
TELEFAX: 416-364-7311
TELEFAX: 416-364-7311
TELEFAX: 416-361-1398
TELEFX: 66-23115
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TTELET AMINO acids
TENTER: AMINO acids
TENTER: AMINO acids
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100.0%; Pred. No. 80;
ive 0; Mismatches
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TELEFAX: 416-361-1398
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-520-933-2
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                         Sequence 45, Application PC/TUS9307306
GENERAL INFORMATION:
APPLICANT: MARGOLIS, Richard U.
APPLICANT: RAUCH, Uwe
APPLICANT: MARGOLIS, Renee K.
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: LOONING, EXPRESSION AND USES FOR A
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APPLICANT: Jefferies, Wilfred A.
APPLICANT: McGeer, Patrick L.
APPLICANT: McGeer, Sylvia
APPLICANT: Rochemberger, Sylvia
APPLICANT: Food, Michael R.
APPLICANT: Food, Michael R.
APPLICANT: Food, Malcolm
TITLE OF INVENTION: Use of p97 and Iron Binding Proteins
TITLE OF INVENTION: as Diagnostic and Therapeutic Agents
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bereekin & Parr
STREET: 40 King Street West
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                                                                                                                                                                                                                                                                             CONTEXTORION ADDRESS:
COUNTRY: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIPE: 20004
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING NOWER: PCT/US93/07306
FILING DATE: 03-AUG-1993
PRIOR APPLICATION NUMBER: US 07/922,911
FILING DATE: G3-AUG-1993
APPLICATION NUMBER: US 07/922,911
FILING DATE: G3-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, GUY K.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MATGOLIS=1A PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
FRNGTH: 17 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
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ADDRESSEE: Browdy an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
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STATE: Ontario
COUNTRY: Canada
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RESULT 44
US-08-834-130A-59
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Sequence 59, Application US/08834130A PALENT NO. 6.180758
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: GILLAM, Shirley
APPLICANT: OU, Dawei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59, Application US/08256747C Patent No. 6037448
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Matches 6; Conserva
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                                                                                                                                                                                                                                                                                                                                     NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/256,747C
FILING DATE: 06-OCT-1994
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCE ADDRESS:
CORRESPONDENCE ADDRESS:
Sim & McBurney
701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 MRGPSG 158
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                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: li
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100.0%; Pred. No.
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100.0%; Pred. No.
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o. 95;
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RESULT 45
US-08-726-306A-118
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 118, Application US/08726306A
Patent No. 5958684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: 14-
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: WordPerfect 6.1
                                          APPLICATION NUMBER: US/08/726,306A FILING DATE: 02-Oct-1996 PRIOR APPLICATION DATA: GB 95/20080.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1038-686 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 14-APR-199
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
               FILING DATE: 02-Oct-1995 PRIOR APPLICATION DATA:
                                                                                                             SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Ontario
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APPLICATION NUMBER:
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                              ADDRESSEE:
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M5G 1R7
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                                                                                                                                                                                                              02111
                                                                                                                                                                                                                                                              Boston
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6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                             1 Financial Center
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VENTION: DIAGNOSIS METHOD AND REAGENTS
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                                                                                                                                                                                                                                                                                                                                                                           Burbach, Johannes Peter Henri
                                                                                                                                                                                                                                                                                             Banner & Witcoff, Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-1997
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US 60/009,832
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5. 95;
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Maximum Match 100%
Listing first 45 s
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                                                                                                        Q9hwl3 pseudomonas
Q51339 pseudomonas
Q9jw26 neisseria m
Q9jxu3 neisseria m
                                                                                                                                                                     Description
                                                                                       Q8zfy6 yersinia pe
Q8x8h4 escherichia
                                                                                                                                                  Q9jxz0 neisseria m
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P72599 synechocyst		16	863	10.6	402	•
Q9jtr6 neisseria m		16	635	10.8	407.5	_
Q8xvbl ralstonia s		16	801	10.9	410	-
Q9ez93 zymomonas m	O	N	762	10.9	410.5	
Q92yc1 rhizobium m		16	714	10.9	411	•
ralstonia		16	689	10.9	412	_
Q8ytv3 anabaena sp	QBYTV3	16	857	11.0	415.5	•
synechoc		16	853	11.0	416.5	_
Q8yuz6 anabaena sp		16	853	11.1	420.5	_
Q8z908 salmonella		16	696	11.2	421.5	
Q926c6 rhizobium m		16	724	11.2	423	•
Q8yuu5 anabaena sp		16	858	11.2	424	
	086424	N	732	11.4	429	-
Q9f0f9 campylobact	o	N	755	11.4	432	
Q9i422 pseudomonas		16	732	11.5	432.5	•
	_	N	732	11.6	436.5	_
pseudomoı	068590	16	753	11.7	441.5	•
		16	872	11.9	449.5	_
		16	819	11.9	450	-
Q8ui89 agrobacteri		16	747	11.9	450.5	
Q93jp3 rhizobium l		N	747	12.1	458	•
	o	N	726	12.1	458	-
Q9hux3 pseudomonas		16	708	٠	459	-
Q8x7w7 escherichia		16	760	12.2	460	
Q8ytx5 anabaena sp		16	851	12.2	460.5	•
Q8xr06 ralstonia s	Q8XR06	16	695	12.3	463	_
synechocy	-	16	828		465	•
Q8ytp0 anabaena sp		16	867	12.4		_
Q926c7 rhizobium m	Q926C7	16	733	12.5	471.5	-

## ALIGNMENTS

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RESULT 1
Q9JX
D1 Q9JX
AC Q9JX

Query Match
                                                                      InterPro; IPR002106; AAtrna_ligaseII.
InterPro; IPR001917; NHtransf 2.
InterPro; IPR001917; NHtransf 2.
InterPro; IPR001931; TonB_boxC; 1.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00599; AA_TRAMSFER_CLASS_2; UNKNOWN_1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
Receptor; Complete proteome.
Receptor; Complete proteome.
SEQUENCE 708 AA; 77068 MW; F3519B024FBBB4EE CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain McCen."
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STRAIN=MC58 / SEROGROUP B;
MEDLINE=20175755; PubMcd=10710307;
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE002532; AAF42164.1; -. TIGR; NMB1829; -.
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NCBI_TaxID=491;
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la; beta subdivision; Neisseriaceae; Neisseria.
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        Score 3244;
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DB 16; Length 708;
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Q8zql0 Q9x6a5 b

0 salmonella bordetella

Q8yv33 Q8ytw7 Q8yxv8 Q8yux0 Q8ymk9 Q8ymk9 Q9ac38

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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Probable TonB-dependent receptor.
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STRAIN=ATCC 15692 / PAO1;
MEDLINE=20437337; PubMed=10984043;
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Bacteria; Proteobacteria;
                     Conservative
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 Local Similarity
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Pseudomonas.
NCBI_TaxID=287;
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

By Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Wastbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saiern M.H., Mancock R.E.W., Lory S., Olson M.V.;

Complete genome sequence of Pseudomonas aeruginosa PAOI, an

Complete genome sequence of Pseudomonas aeruginosa PAOI, an

Nature 406:999-964(2000).

RMBL, ABO04033; AAG0755.1; -.

RMBL, ABO04033; AAG0755.1; -.

R InterPro; IPRO0531; TonB_boxC.

Pfam: PF00593; TonB_boxC.

Pfam: PF00593; TonB_boxC.

R Receptor; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 KQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGL---ALNEFRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPOVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE
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                                                                                                                                                                                                                                                                                                                                                                                                         72;
                                                                                                                                                                                                                                                                                                                                                                    Length 802;
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                                                                                                                                                                                                                                                                                                                                                            Query Match 22.0%; Score 832; DB 16; Best Local Similarity 30.0%; Pred. No. 9.6e-41; Matches 222; Conservative 137; Mismatches 309;
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Best Local Similarity
Matches 217; Conserv
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CONFLICT
SEQUENCE
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Q51339;
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McMorran B.J., Merriman M.E., Rombel I.T., Lamont I.I "Characterisation of the pvdE gene which is required synthesis in Pseudomonas aeruginosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Merriman T.R., Merriman M.S., Lamont I.L.;
"Nucleotide sequence of pvdD, a pyoverdine biosynthetic gene
"seudomonas aeruginosa; PvdD has similarity to peptide synthe
J. Bacteriol. 177:252-258(1995).
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Poole K., Neshat S., Krebes K., Heinrichs D.B.;
Poloring and nucleoride sequence analysis of the ferripyoverdine receptor gene fpvA of Pseudomonas aeruginosa.";
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01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=PAO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=PAO;
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                                                                                                                                                 LTPRETPQSITVVTRONMDDFGLNNIDDVMRHTPGITVSAYDTDRNNYYARGFSINNFQY 219
LNPDTMLTVGADYQDNDPKGSGWSGSFPLFDSQGNRNDVSRSFNNGAKWSSWEQYTRTVF
                      INPDTVLGAGYLYQQRHL--APYNG-LPA-DANNKLPSLPQHVFVGADWNKFKWNSHDVF
                                               HVELGAGSWDNYRSELDVSGPLTESGNVRGRAVAAYQDKHSFMDHYERKTSVYYGILEFD
                                                                      HAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWD
                                                                                                DGIPSTARNVGYSAGNTLSDMAIYDRVEVLKGATGLLTGAGSLGATINLIRKKPTHEFKG
                                                                                                                        DGLPAQMQSI----NGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQG
                                                                                                                                                                          ASLREIPOSVSIITNOOVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
                                                                                                                                                                                                     FQGNAITISVAEAADSSV-----DLGATMITSNQL--GTITEDSGSYTPGTIATATRLV 159
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Last annotation update)
                                                                                                                                                                                                                                                     Score 821.5; DB 2;
Pred. No. 4.1e-40;
5; Mismatches 312;
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Y -> F (IN REF. 1).
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Best Local S
Matches 232
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                                                                                                                                                                                               Parkhill J., Achtman M., James K.D., Bentley S.D., Churche Klee S.R., Morelli G., Basham D., Brown D., Chillingworth Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseri"
                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis (se
Bacteria; Proteobacteria;
                                                                                                                                             EMBL; AL162753; CAB83866.1; InterPro; IPR000531; TonB_b
                                                                                                                                                                                                                                                                                                           STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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01-OCT-2000
                                                                                                                     Receptor;
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                                                                                                                                Pfam; PF00593;
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 MTRFKYSLLFAALLPVYAQADVSVSDDPKPQESTELPTITVTADRT-----ASSNDGYTV
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                                                                                                                                                                       404:502-506(2000).
                                                                Similarity
                                                                                                        Complete
725 AA;
                                                   Conservative
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                                                                                                                                 TonB_boxC;
                                                                                                      proteome.
80302 MW;
                                               20.9%; Score 788; DE
29.9%; Pred. No. 3.2¢
tive 117; Mismatches
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beta subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADD 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYA 407
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                                                                                                                   115 VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
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STRAIN=MCSB / SERGGROUP B;
MEDLINB=20175755, PubMed-10710307;
MEDLINB=20175755, PubMed-10710307;
MEDLINB=20175755, PubMed D.W., Peden J.F., Dedson R.J.,
Nelson J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson M.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                SGTHTPLGLPMTLREIPQSVSVITSQQMRDQNIKALDRALLQATGTSRQIYGSDRAGYNY
                                                                                                                                                   - NIYYRAANQAKTHGWEIEVGGRITPEWQIQAGYSQSKTRDQDGSRLNPDSV----PERS
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(TrEMBLrel. 19, I
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TonB-dependent receptor
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NCBI_TaxID=491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYAR 408
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                                                                                                                                                                                                                MSVFRINMTAATVL-----AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSS 57
                                                                                                                                                                                                                                                                     SGTHTPLGLPMTLREIPQSVSVITSQQMRDQNIKTLDRALLQATGTSRQIYGSDRAGYNY
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'Complete genome sequence of Neisseria meningitidis serogroup
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                                                                                                                                         Length 725;
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                                                    TIGR; NMB1882; --
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
Sceptor; Complete protecme.
SEQUENCE: 725 AA; 80478 MW; D3953D4485FD8FAF CRC64;
                                                                                                                                      Query Match
20.8%; Score 784; DB 16;
Best Local Similarity 29.4%; Pred. No. 5.5e-38;
Matches 228; Conservative 118; Mismatches 320;
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Science 287:1809-1815(2000)
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Best Local Sim
Matches 223;
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STRAIN=CO-92 / BIOVAR ORIENTALIS;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Prentice M.B., Sebaihia M., James K.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Leather S., Moule S., Oyston P.C.F., Quail M., Sutherford K.,

Leather S., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ414149; CAC90360.1; -. InterPro; IPR000531; TonB_boxC. Pfam; PF00593; TonB_boxC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01156; TŌNB_DÉPENDENT REC 2; UNKNOWN 1.
Receptor; Hypothetical protein; Complete proteome.
SEQUENCE 753 AA; 83838 MW; 739512F31D328166 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=632;
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ARVSFYRMKDKN-----AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFNCTHPIKPAAWVLAANVSLLGCAYAATDENNSQKKERENNPANTTITVTASPLRHAGV
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                                                FVPYSGLTYDINRDLSVYTSYTEIFNPENRRDRNNTLLAPVSGQNYEAGLKGVAFDNSLD
                                                                            FTGYAGAVYDLINDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLN
                                                                                                                                                                            LGWNRQRQNIDNDYYLAT-----CNATRTCPDLGDFTQPGWQYPKPVWSDKRAYGSK
                                                                                                                                                                                                          IGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQV-----
                                                                                                                                                                                                                                         YPDPQTNIGM-----RPGSLSLIDGA-----RRQQNYDIQVNGQYSLFGRQHQLG
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                                                                                                                                                                                                                                                                                                     GRTNYAQSATTASDWASAETRTQTLFSSLQHNFDN-GWNIKGTFTFDNDKLRQDVMWPTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEDSGSYNTSSMSTATGLNISARETPOSVSVLTKORMRDONLNSVESAVNNITGISVROF
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Conservative 136; Mismatches
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Pred. No. 2.
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Best Local S
Matches 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8X8H4;
Q8X8H4;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00430; TŌNB_DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1.
Receptor; Complete proteome.
SEQUENCE 729 AA; 81231 MW; BBF5ADA133F0595B CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R., Welch R.A., Blattner F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=0157:H7 / EDL933 / ATCC 700
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                              QYQAITKPSLLAGCIALALLPSAAFAAPATE-ETVIVEGSAT---APDDGENDYSVTSTS
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YSEYNIDGLPAQMQS---INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT
                                              AGTKMQMTQRDIPQSVTIVSQQRMEDQQLQTLGEVMENTLGISKSQADSDRALYYSRGFQ
                                                                                          VGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYE 121
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                                                                                                                                                                                                                                                211;
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Last annotation updat
ferric iron uptake.
                                                                                                                                                                                                                                                                       Score 736.5; DB 16; Pred. No. 3.4e-35;
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                                                                                                                                                                                                                                                                                                                                               BBF5ADA133F0595B CRC64;
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                                                                                                                                                                                                                                             Indels 105;
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01-JUN-2002 (TrEMBLrel. 20, Last sequence update)
Outer membrane receptor 121, Last annotation update)
and Fe/III)-rhodotrulic acid uptake.
FHUE OR STW1204
Salmonella typhimurium.
Bacteria; Profect
363 GFDYVGGTGWNSGKRKVDALDLFADGSYELFGROHNLMFGGSYSKONNRYFSSWANIFPD
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                          Query Match 19.1%; Score 721; DB 16; Length 7
Best Local Similarity 27.7%; Pred. No. 2.8e-34;
Matches 208; Conservative 137; Mismatches 321; Indels
                                                                    94622BFE3714BFC2 CRC64;
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PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1 PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1
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EMBL; AF135154; AAD26430.1; -.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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"Essential role of the iron-regulated outer membrane receptor FauA alcaligin siderophore-mediated iron uptake in Bordetella species.";
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                                                                                                                                                                                                    PRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAA-----APLNPNNKKTRYAALGKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVSPILSQWNYGSTDMDAAIYDHVEIVRGATGLMTGSGNPSAAVNFVRKRPLREFAATFN
DKKYYDQIG
                           NRHYYARVG
                                                         ALHRLTVGGGVDWQSRMYQAAASPRGNVEVEQDSYALVSLMARFDFNKKLSATLNVNNLF
                                                                                      -TPELTIGGGVNAMSGITSSAGMHAG------GYATFDAMAAYRFTPKLKLQINADNIF
                                                                                                                      V-EGIDLEASGQILEDWNI--GASYTHETTKDASG---NPINTNHERSLEKLYTTYRLEG
                                                                                                                                                     VMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQV--
                                                                                                                                                                                    PIKSKSYELGLKAAYLEGRUNTSAALFQTRQDNLAQVIPGSSIPGFPNMQASR-AASGAK 590
                                                                                                                                                                                                                                                  SDWKTKQMYFGSRREYRIKNQFTPYAGLTYDINDTYTAYASYTEIFQPQNARDTSGGILP
                                                                                                                                                                                                                                                                                GHYKIESGE-GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLK 528
                                                                                                                                                                                                                                                                                                               ----PAIGSFFDWRRAHIQEPSWADTLSPADDVRTKQTGAYLVGRFALAEPLHLIVGDRW 471
                                                                                                                                                                                                                                                                                                                                             FRSIPQVDLIANARKG---VRGYSHTVATEN---LDEFGIYGKSTFHPADGLSLIGGGRL
                                                                                                                                                                                                                                                                                                                                                                            ----NLDRDDIHF--SLSAPFEAFGLRHEVALG----WMSIDNHSDIQRYAMVGPA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                         YFVDLTHRFTNDWKLRAAYSHTDGRYLMKHVYRGGYPDRHTGIIAAPPAFSNYDG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTVLTTSVEYQHNHSNGFGSGFPLFYSDGSRTDFNRSVAN-----NAPWARQDTEATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTVLGAGYLYQQRHLAPY-NGLP-----ADANNKLPSLPQHVFVGADWNKFKMNSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASVGSWDYVRGDADISVPITEDGRIRSRLVAAYSQGDSYVHFLDTRRRTFYGVVSADLTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPAQMQS---INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRETPQSVSVVTRQQIEDQGLTDTGAILATAPGISVTRSDSNRYSFSARGFTIDNFQFDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LREIPOSVSIITNOOVKORNVOTFOQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNIDG 129
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                             700
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Pred. No. 1.9e-30;
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Best Local Similarity
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01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21595285; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yabada S.; "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP003588; BAB73847.1; -.
InterPro; IPR0005106; AATRNA_ligaseII.
InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB boxC; 1.
PROSITE; PS00339; AA TRNA_LIGASE_II_2; UNKNOWN_1.
Receptor; Complete proteome.
Receptor; Complete proteome.
SEQUENCE 863 AA; 95445 MW; 40F9EC04FE462D34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc
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LNARVSFYRMKDKNAAAPLNPNNKKTRYAAL-----GKRVMEGVETEISGAVTPKWQIH
                                                                                                                                                  GYSH---TVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE---GKTLHKASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVL 106
                                                     SAFSPRIGLVYQPSKSVSLYTSYSQSFVPETGVNPDGEIFEPTRGTQYEAGIKADFLEGR
                                                                          TKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDR : | : | | : | : | | : | | | | | | : : : |
                                                                                                                             SFDYGPRSSSTERFQTYG1YLQDQ1TFLDNLKLL1GGRFDW1SGENTDNVTGDTTQNPDS
                                                                                                                                                                                                   GKFNTGSISHQILIGFDFNHNIDT
                                                                                                                                                                                                                                                                           NNFSVVTSK------NAEEYTLATGVVNDQSLRQFAQDREFTQDNYFGQIDLL
                                                                                                                                                                                                                                                                                                             SNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSR-----
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                                                                                                                                                                                                                                       - PFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVR
                                                                                                                                                                                                                                                                                                                                                 -NTFLPRSFYQAYPNNAYVDNTTQKL
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2 (TrEMBLrel. 21,
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25.0%; Pred.
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No. 6.8e-22;
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ima K., Kimura T.,
A., Muraki A.,
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(TrEMBLrel. 20, C
(TrEMBLrel. 20, I
(TrEMBLrel. 21, I
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Matches 179; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 AGLILAVESTITATOPPATPISDAPPAEPIAOODDPIELVVIGEODRYRVPIASTATKID 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGLPAQMQSING-----TLPNLFAPDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 FOGHAAAGFGTHKQYKAEADVSGSLNSDGSV--RGRVMAQTVGASPRPAEKNNRHETFYA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - AADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGL 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
682 LSATLAAYQITKSNILTP-DPDPER---AALDYLIQVGEQRSRGIELDVAGEILPGWKAI 737
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                           AGYSYLHSQIKTASNSRDDGIFLL-MPKHSANLWTTYQVTPE----LTIGGG---VNAMS
                                                  738 ASYAYINAEV-TEDNDIPVGNRLVSVPKNQASLWTTYEFQNSDLKGLGFGLGLFYVGTRS
                                                                                              MEDLINE=21995285; PubMed=11759840; Kaneko T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yabata S., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
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Best Local Similarity 24.6%; Pred. No. 2e-20;
Matches 185; Conservative 112; Mismatches 353; Indels 103;
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INTERPRO, IPR00531; TonB_boxC.
Pfam, PF00593; TonB_boxC; 1.
Receptor; Complete proteome.
SEQUENCE 820 AA; 91035 MW; BBD0B2486468C451 CRC64;
                                                                                                                                                                                                                                                        (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                               820 AA.
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing 12.9%; Score 486.5; DB 16; Length larity 23.9%; Pred. No. 2.2e-20; Conservative 117; Mismatches 343; Indels Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc. Complete proteome.
RAS AA, 98141 MW; AF7F6BAE0A37FE08 CRC64; Last sequence update) Last annotation update) EMBL; AP003584; BAB73058.1; ...
InterPro; IPR001064; Crystallin.
InterPro; IPR0010531; TonB\_boxC.
Pfan; PF00593; TonB\_boxC; 1.
PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1. cyanobacterium Anabaena sp. strain PCC 7120."; 690 IENRHYYARVGGANTFNIPGSERTWTANLRYSF 722 789 LFNETYYETSOARNTI-YPGAPFTVIGSFSIOF Created) PRT; Anabaena sp. (strain PCC 7120)

183; Conservative

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Pred. No. 3.2e-20;
4; Mismatches 328;

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                                                                                                                                                                                SEQUENCE FROM N.A.

MEDIINE=11595285; PubMed=11759840;

Kaneko T. Nakamura Y., Wolk C.P., Kuritz T., Sasamo Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Mur Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yan Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrog: Cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).
     Query
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01-MAR-2002
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PF00593; TonB boxC; 1.
tor; Complete proteome.
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  MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Watanabe A., Iriguchi M., Ishikawa
                                                                                                                                                               Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              Ferrichrome
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 858;
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                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%; Score 481; DB 16; 25.2%; Pred. No. 4.5e-20;
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851 AA

PRT;

PRELIMINARY;

Q9AC38 Q9AC38; RESULT 15 Q9AC38 ID Q9AC36 AC Q9AC36

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STATN=ATCC 19089 JUMPd=11259647;

A MEDLINE=21173699 PubMed=11259647;

A Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Decocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

Deboy R.T., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

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12.7%; Score 479; DB 16; Length 851;
Best Local Similarity 24.7%; Pred. No. 5.8e-20;
Matches 198; Conservative 126; Mismatches 341; Indels 138;
                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
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Pfam; PF00593; TonB_boxC; 1.
Receptor; Complete protecome.
SEQUENCE 851 AA; 90124 MW; B75B166237FC5D92 CRC64;
Created)
Last sequence update)
Last annotation update)
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(TrEMBLrel. (TrEMBLrel.
                                                              (TrEMBLrel.
                                                                                          TonB-dependent receptor
                                                                                                                                                         Caulobacter crescentus
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Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaca sp. strain PCC 7120.";
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Watanabe A., Iriguchi M., Matsumoto M., Matsuno A., Muraki A.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
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Bacteria; Cyanobacteria; Nostocales;
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                                                 FAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIG
                                                                                                                                                  PSL----PQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYS----DRDADSNYA
                                                                                                                                                                                                         NASYEKADNFVDFNDRENFSVASTLSFALGENTTLTLDQEYNKVNQGYYNGVPA-VGTVL
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863 AA; 95343 MW;
LDPDQRTLQRGVQDADDRYQTYDLSTNVVGK---
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Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

EMBL; AL591790; CAC46802.1; ...
                                                                                                                                                                                                                                                                                                                                               Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux (Bodrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puchler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
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0926C7; PRELIMINARY;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                        Pfam; PF00593; TonB_boxC;
Complete proteome.
SEQUENCE 733 AA; 79611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                    InterPro; IPR000531; TonB_boxC. Pfam; PF00593; TonB_boxC; 1.
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                            SEYN--IDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
                                                                                                                                                         MTAATVLAALSSSVFA----AQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP
AQTGLFLDGLPLFSFGFGNFQVDPFMLERVEVLKGPASVLYGGSNPGGIINLISKRPLDE
                                                                                                                           LASGVALAPLMMSGIALAQEGNATQLERIVVEGGNAAGASATGPVDGYVAKATATGSKTA
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E 733 AA;
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                                                                                                                                                                                                                                                                                                                                MKDKNAAAP---LNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKT 613
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FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVWAQTVGASPRPAEKUNRHETFYAAA 240
                                                                                                                                         336 MKTPAGRPGCNTADDKAC-AVGLGTEIKQKALAPDASYSRPFRLGNTANBFVIGADYNRF 394
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                                                                                                                                                                                                                                                   GKSTFHPADGLSLIGGGRLGHYKIESGEG-KTLHKASKTKFTGYAGAVYDLNDNNSLYLS
                                                                                                                                                         241 DWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQ-HV-----FVG----ADWN
                                                                    240 SEDLR-----GFILPQVTYAPDDATSLTVFGLLQSLDQVHVGNGFLPYVGTVEDAPFG
                                                                                            290 KFKMNSHDVFADL------KHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLG
                                                                                                                   293 KIDRDAYYSEPÜIDEGSYTQQMLGYEFKHDFDNGWTFTQNARYANLHKHEKYPYTYGYVĞ
                                                                                                                                                                                       RSTNEQ---GRITLYARGGLALNEFRSIPQ-VDLIANARKGVRGYSHTVATENLDEFGIY
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikwa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Kaneko T., Sato S., Sotani H., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Okumura S.,
Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Yamada M., Yasuda M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEISGAVTPKWQIHAGYSYLHSQIKTASNSR-DDGIFLLMPKHSANLWTYQVTPELTIG 646
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TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA--- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                             371 SYSRPFRIGNTANEPVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLI--ANA
                                                                                                                                                                                                                                             -DANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDR---DADS
                                                                                                                                                                                                                                                                                                                      422 RETNLGEPSLSE------SESLVTRL------GY-QLDHRLNDNWTIKSEF
                     ----RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLV
                                                                                                         256 TPVIRGFESRNLLRNGLRDDSLRFQSEIANV---ERVEVLKGPASVLFGQGDLGGVVNLV
                                                                                                                                                                      --NNRHETFYAAADWDI--NPDTVLGAG--YL-YQQRHLAPYNGLPA------
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Bacteria; Cyanobacteria; Chrococcales; Synechocystis
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ENYYE---GARDIVRVIPGAPFTLTGSVSFEF
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Best Local :
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EMBL; D90899; BAA16602.1; -.
InterPro; IPR000531; TonB_boxC.
Pfam; PF005531; TonB_boxC; 1.
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VGKIGVTF
                              TANLRYSF 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSLTSSSTAIAPENPESEIEVV------ATQEGQGEASYFVPSASTATGLDTPLL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLAALSSSVFAA---QTADLETVHIKGQRSYNAIVTEKNGDYSSF--AVTVGTKIPASLR 71
                                                            DNTFVLPSYFRTDAAIFYR-RENWELQLNIENLFNTQYLAE---SNDFDLSVYPGAPFTV
                                                                                     -----GYATEDAMAAYRETPKLKLQINADNIENRHYYARVGGANTENI---
                                                                                                                                                                                                                                                       YQPIPTVSLYGSYTTSFNPSFAASLNADGSTFDPQTGRQFEVGVKAD-ITDKLSVTFSAF
                                                                                                                                                                                                                                                                                   YDLNDNNSLYLSLSQLYTPQ--TNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFY
                                                                                                                                                                                                                                                                                                                                                                                                                 EQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHT---VATE----NLDEFGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FÜEDT-----GELNRFEYYGGGNYORFFTNAELIGEFYTGPVKHRVLFGLEYRNDTETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSKFEQDQYLIGYTFNHDFNENLKLRHAMQY-----LAYAPVRYA-----PLFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TLTWNIGPDTKLNIYGQYTTNRETLDEGIPAP---NIADLPSNRFLGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFRDGIPYQSLAPLNTT-----DIEQIEVLKGPSSIVFGAGEPGGSINLISKKPLDEPYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315D8491FA82FEE3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L. Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Deman Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearu Nature 415:497-502(2002).

EMBL; AL646082; CAD18213 1; -.
InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB boxC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBXR06 PRELIMINARY; PRT; 695 AA.
QBXR06;
QBXR06;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation updat probable ferrisiderophore receptor protein.
RSP1062 OR RS02469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid; Complete proteome. SEQUENCE 695 AA; 75590 MW;
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STRAIN=GMI1000;
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DGKLLKPROGNQFEVGYKGSYMDDRLNARVS--FYRMKDKNAAAPLNPNNKKTRYAA-LG
                                                QSRDDLTPKNQDLSRTDK-PVSPRLGIVYHPVEALSLYASYSRSFQPLADSFTYYTNSSA
                                                                                                                                                                                   LTQQAETFGIRHTLLYGIELGYQDKSDRVAA-----
                                                                                                              VPVVLPTVPANATPSNYGLTHN-----ETYAMYAQDLIKFSPQWTVLAGLR---YEVLK
                                                                                                                                                                                                               IKQKALAFDASYSRPF--RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRS
                                                                                                                                                                                                                                                                                 LKHYFGN-GGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTE
                                                                                                                                                                                                                                                                                                                                                                                  EGOKRAEFDLNTSINDDA-----VRARLTGAVEDSGGFRNDYFLRRQAISPSFLFNLSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I PQSVNVVPRAVIQDQGALSLNDTLRNVPGVSASLGDAQRDQVTIRGFSAINDQYVDGLR
                                                                                 ESGEGKT-----LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTP-----QTNLDA
                                                                                                                                               IPQV--DLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKI--
                                                                                                                                                                                                                                                  LDHRINDQWSFHSVVRNYEYALGRNNYVTVSRVTGGAVPTVTLGVNQRNRSDRGTVWQNE
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                                                                                                                                                                                                                                                                                                                  TKLTLQFDYLHDTRIADQGVPSYRGRPVN----VPIETRYGSANAGDGNVETTVKSVTGT
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01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
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814 GLNFKNIFDVNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MQSINGTLPNLFAFDRVEVBVMRGPSGLFDSSGEMGGIVNLVRKRPTK---AFQGHAAAGFG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRS--SVYARGY-EYSEYNIDGLPAQ 133
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----LAPQSTTNYEIGAK---YDVSASASVSAALFDMKQTN----LTSVDPATQLAVPIG 545
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                                                                      WTTYQVTPELTIGGGVNA------MSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQIN
                                                                                   KRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL-----LMPKHSANL
                                      MEDLINE=11955985; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Watanabe A., Iriguchi M., Ishikawa A., Rawashima K., Muraki A., Rishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto G., Takazawa M., Tabata S., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316; Indels 123;
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Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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SEQUENCE 851 AA; 93901 MW; 5F93DD9E558D291D CRC64;
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Best Local Similarity 23.6%; Pre
Matches 173; Congervative 120;
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EMBL, AP003590; BAB74287.1; -
InterPro, IPR00531; TonB_boxC.
Pfam; PF00593; TonB_boxC, 1.
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12:";
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STRAIN-CIST.H7 / EDL933 / ATCC 700927;
STRAIN-CIST.H7 / EDL933 / Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Kirkpatrick H.A.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rosela G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Melch R.A., Blattner F.R.
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                                                                                                                      LKPRQGNQPEVGYKGSYMDDRLNARVSFYRMKDKNAAAP----LNPNNKKTRYAALGKRV
                                                                                                                                                                                                                                                                                                                   583 MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL-LMPKHSANLWTTYQVTP
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GLALNEFRS I PQVDLI ANARKGVRGYSHTVATENLDEFGI YGKSTFHPADGLSLIGGGRL
                                                                                                                 GHYK----IESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKL
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EMBL, AP002553; BAB34306.1; -.
InterPro; IPR000531; Tona boxc.
PROSUS; Tona boxc; 1.
PROSITE; PS00430; TONE DEPENDENT_REC_1; UNKNOWN_1.
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MEDLINE=21156231; PubMed=11258796;
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SEQUENCE FROM N.A. STRAIN=ATCC 15692 MEDLINE=20437337;
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01-MAR-2001 (TrEMBLrel. 16, Last
01-MAR-2002 (TrEMBLrel. 20, Last
01-MAR-2002 (TrEMBLrel. 20, Last
probable outer membrane protein.
                                                        NCBI_TaxID=287;
                                                                                           Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
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 PubMed=10984043;
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
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 VNVNNLFDRRYYER-SYNNVWVAPGEPRNLTMSLTLNY
                  INADNI FNRHYYARVGGANTFNI PGSERTWTANLRYSF
                                                                                                                                                   KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA
                                                                                                                                                                                        FKPNGGTDMAGKAFDPEEGRGYEAGVKLDLLDGRLGMTLAAFHLKKKNVLTADPSNPGYQ
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                                                                                                                                                                                                                                                                                   SLIGGGRLGHY-----KIESGE-GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                 GTEIKQKALAFDASYSR-----PFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLA 412
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                                                             SLMGVYEFREGWLHGADAGAAVNYVGERAGDSSDSGFELPAYTTVDLLARYPLASNATLG
                                                                                           NLWTTYQVTPELTIGGGVNA-----MSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQ
                                                                                                                          QT----AGEARSQGFDLQFSGQLTEQLRLIGAYAYIDAEVTKDENIARGSRLLNVPKHSG
                                                                                                                                                                                                                     YTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN--AAAPLNPNNK
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Pred. No. 6.7e-19;
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STRAIN=8401 PRL1;
MEDLINE=20244627; PubMed=10784041;
MEDLINE=20244627; PubMed=10784041;
Veoman K.H., Wisniewski-Dye F., Timony C., Stevens J.B., deLuca N.G.,
Downie J.A., Johnson A.W.B.;
"Analysis of the Rhizobium leguminosarum siderophore-uptake gene
fluA.differential expression in free-living bacteria and nitrogen-
fixing bacteroids and distribution of an fhuA pseudogene in different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTPAGRPGCNTADDKACAVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRS 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 GTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSN--DDGRSSVYARGY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 GEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVWAQTVGAS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||:||:||:||:|||:
GSPGGLVNKISKLPTEEPIHEVGISYSTKDRAQAMFDFGGPI-SEGN--DDFLYRIVGLA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TVAHRNASSIRDE----- 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 TNEQGRITLYARGGLALNEFRSIPQVDLIANARKGVRG----YSHTVATENLDEFGIYG- 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 -------EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 -RHGDNNFDIADDRYFLAPSFTWKPDEGTSFTLYG---LAQSDETDANVGAITTVDGKIL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 SLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGM 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 MTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFAV---TV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 PRPAEKN--NRHETFYAAADWDINPD----TVLGAGYLYQQRHLAPYNGLPADANNKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 DIRQS---DPDYDYQKVKQQQIGYQFEHEFDNGLIFRQNLRYSHLDLRARYLGVSSWTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 NITTVGDYRDSLRQPYINYGMFRTD--PYQLQ-------RVEVIKGPVSVLYGS
                                                                                                                                                                                                                                                 Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Rhizobiaceae, Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313; Indels 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 37 POTENTIAL.
726 AA; 79499 MW; BDEBFZA5CSAA0408 CRC64;
                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                       Outer membrane siderophore receptor precursor
                                                                       726 AA
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                                                                                                                     Created)
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Pfam; PF00593; TonB_boxC; 1.
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Microbiology 146:829-837(2000)
EMBL, AJ238208; CAB41037.1;
HSSP; P06971; 10J0.
                                                                                                                01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20,
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                       Rhizobium leguminosarum
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                                                                                                                                                                                                                                                                                                     NCBI_TaxID=384;
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                          RESULT 2

OSYX79

ID QOXXX9

OD AC QO93

BOT O11-

DD O11
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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| GSPGGLVNKISKLPTEEPIHEVGISYSTKDRAQAMFDFGGPI-SEGN--DDFLYRIVGLA 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     607 LHSQIKTASNSRDDGIFLLMPKHSANLWTTY---QVTP--ELTIGGGVNAMSGITSSAGM 661
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FTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYM---DD
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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01-MAR-2002 (TrEMBLrel. 20, Last at
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FHUA.
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01-JUN-2002
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Science
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Wood D.W., Setubal J.C., Kaul R., Monke D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Romero P., Gordo
Raymond C., Rouse G., Saenphimmende C., Wu Z., Romero P., Gordo
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
Meetre P.
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullir Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
                                                                                                                                                                                                                                                                                                         Nester
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                                                                                                                                                                                           SEQUENCE FROM N.A.
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Science 294:2323-2328(2001).
EMBL; AE009012; AAL41430.1; ALT_INIT
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                          AGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNI PGSERTWTANL
                                                                                  YLHSQIKTASNSRDDGIF-LLMPKHSANLWTTYQVTPE----LTIGGGV--NAMSGITSS
                                                                                                              GSITASV-FKLVKD-NAIVSYTAGGVTTS-GQFGQVESTGFELEAKANLDENWKALASYS
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MEDLINE=2160856; PubMed=11743193;

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Rang G., voo H., Tao Y., Biddle P., Jung M., Kreeppan W., Perry M.,

Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
11.9%; Score 450; DB 16; Length 819;
Best Local Similarity 25.5%; Pred. No. 2.8e-18;
Matches 187; Conservative 106; Mismatches 349; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89022 MW; 976C509F6DE91628 CRC64;
                  Agrobacterium tume faciens (strain C58 / ATCC 33970)
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EMBL, AE007900, AAK80685.1; ALT INIT.
Plasmid; Receptor; Complete proteome.
SEQUENCE 819 AA; 89022 MW; 976C50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 294:2317-2323(2001).
                                                                                                  Rhizobiaceae; Rhizobium
ATU5311 OR AGR PAT
                                                                                                                     NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nester E.W.;
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                                                                                  574 KIDTAFTGRAGLIYLFDNGFAPYVSYSTSFMPYSGFDGQNNPFKPTTGEQWEVGLKYEPV 633
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522 PTVGARW-----DNRISQLGLYAQDQI-KWDNWILTLGGRY-DWALQTDNDILSSTIGK 573
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In DNA Res. 8:205-213 (2001).

REMBL; AP003590; BAB74325.1; -.
RINTERPO; IPRO01484; Pyrokinin.
RINTERPO; IPRO00531; TonB boxC: 1.
R PF00593; TonB boxC: 1.
R PROSITE; PS00599; PYROKININ; UNKNOWN_1.
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                                                    485 ASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYM
                                                                                                                                                       545 DDRLNARVSFYRMKDKNAAAPLNPNNKKTRY--AALGKRVMEGVETEISGAVTPKWQIHA
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Bacteria, Cyanobacteria, Nostocales; Nostocaceae, Nostoc
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SEQUENCE 872 AA; 95972 MW; 6485E569DBEA3E61 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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O68590;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYDROXAMATE-type ferrisiderophore receptor (Iron transport protein
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE=9621057; PubMed=9633080;

Ochsner U.A., Vasil M.L.;

"Gene repression by the ferric uptake regulator in Pararuginosa: cycle selection of iron-regulated genes."

Proc. Natl. Acad. Sci. U.S.A. 93:4409-4414(1996).
                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=ATCC 15692 / PAO1; Ochsner U.A., Vasil A.I.,
                                          Schwan W.R., Barker L., Brody L.L.;
"Differences in sensitivity to PA-1806 among iron transport Pseudomonas aeruginosa compared to Escherichia coli."; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
  SEQUENCE
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                            Submitted (MAR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
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EMBL; AP051690; AAC06215.1; --

EMBL; AP276976; AAR897743.1; --

EMBL; AB004865; AAG07902.1; --

InterPro; IPR000531; TonB boxC; --

Ffam; PF00593; TonB boxC; --

Receptor; Complete proteome.

Receptor; Complete proteome.

SEQUENCE 753 AA; 82336 MW; 4DD5430DC9D6514B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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                                             TTYQVTPELTIGGG---VNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIF
                                                                                                         ADISVGNNGLDPERNRNLELGTKWAFFDDALSLNAALFR-TDKTNARVASP-DVSTLQVL
                                                                                                                                      TNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAA
                                                                                                                                                                      GPAGYFKRE-----NNSHFWNYQTGLVYKPAPNGSIYLAWSTSSNPTGETGGEGQ
                                                                                                                                                                                                     GRLGHYKIESGEGKTLHKASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-YSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTK 179
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22.9%;
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Pred. No. 7.
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NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 165; Gaps
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TTYDLLQNFTIGGGTTYVDKQYGNTANS-TYIPSYWRYDAMASYKVSKNVDLQLNVQNLT 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
11.6%; Score 436.5; DB 2; Length 732;
Best Local Similarity 23.3%; Pred. No. 1.5e-17;
Matches 178; Conservative 123; Mismatches 299; Indels 165;
                                                                                                                                                                                                                                                                                           Pseudomonas
                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                           Ochsmer U.A., Vasil A.I., Johnson Z., Vasil M.L.;
Ochsmer U.A., Vasil A.I., Johnson Z., Vasil M.L.;
Genetic characterization of novel siderophore receptor (in iron acquisition in Pseudomonas aeruginosa.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR055693; AAC06225.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                732 AA; 80898 MW; 1E7AE28338B4DAD6 CRC64;
                                                                                                                                                                                                                                                                            Ochsner U.A., Vasil M.L.;
"Gene repression by the ferric uptake regulator in Psel aeruginosa: cycle selection of iron-regulated genes.";
Proc. Natl. Acad. Sci. U.S.A. 93:4409-4414(1996).
                                                                                                                                         Last sequence update)
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Pfam; PF001593; TONB_boxc; 1.
PR0SITE; PS01156; TÖNB_DEPENDENT_REC_2; UNKNOWN_1.
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PFUA.
                                            692 NRHYYARVGGANTFNI-PGSERTWTANLRYSF
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MEDLINE=96210657; PubMed=8633080;
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                                                                                                               PRELIMINARY;
                                                                                                                                                                                             Pseudomonas aeruginosa
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SEQUENCE
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STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; Pubmed=10984043;

Stover C.K., Pham X.-Co.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Co.T., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino B., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S, Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Reizer J., Saier m.H., Hancock R.E.W., Lory S., Olson M.V.; Romer Complete, genome sequence of Pseudomonas aeruginosa PAO1, an
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----RT-----TLYARGGLALNEFRSIPOVDLIAN 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 538 GYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPK
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                                                                                                                                                                                                                                                                            459 LRYDWIDGTSRSTPS-----GKPT--------VRADSSDG-----
                                                                                                                                                                                    428 AR-KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKAS
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Best Local Similarity 23.3%; Pred. No. 2.5e-17;
Matches 178; Conservative 123; Mismatches 299; Indels 165;
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EMBL, AE004561; AAG04711.1; -.

InterPro; IPR006531; Tonn boxC.

Pfan; PF00593; Tonn boxC; 1.

PROSITE; PS01156; TÖNB_DEPENDENT_REC_2; UNKNOWN_1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequel-001-007-2001 (TrEMBLrel. 18, Last annuprobable TonB-dependent receptor.
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SEQUENCE 732 AA; 80835 MW;
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                                  389 ADY -- NRFRSTNEOG----
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Pseudomonas aeruginosa
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Query Match
Best Local Sin
Matches 179;
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                                                                                                                                            "Cloning
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-21064758; PubMed=11136137;
MEDLINE-21064758; PubMed=11136137;
Galindo M.A., Day W.A., Raphael B.H.,
"Cloning and Characterization of a Ca
                                                                                                                                       Operon.
                                                                                                                                                                                                                Campylobacter.
NCBI_TaxID=197;
                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                        Campylobacter jejuni
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                                                                       Microbiol. 42:139-143 (2001)
AF241226; AAG47637.1; -
P06971; 1BY5.
Pro; IPR000531; TonB_boxC.
PF00593; TonB_boxC; 1.
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             Similarity
                                                   755
 Conservative
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                                                  83851 MW;
11.4%; Sc
23.9%; Pr
tive 116;
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Score 432; DB
Pred. No. 2.8e
16; Mismatches
                                                  C4140C3D258202E0 CRC64;
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                                                                                                                                                   f., Joens L.A.;
Campylobacter
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           DB 2;
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                      Length 755;
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Indels 124;
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RESULT
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a; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 THKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVL
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    coli, Salmonella paratyphi
                                                                                                                                                                                                                                   Length 732;
                                                                                                                                                                                                                              Query Match
11.4%; Score 429; DB 2; Length 73
Best Local Similarity 23.7%; Pred. No. 4.1e-17;
Matches 172; Conservative 105; Mismatches 356; Indels
                                                                                                                                                                                        8706DFAA883BC190 CRC64;
                     Salmonella typhimurium, and Panteea agglomerans."; J. Bacteriol. 180:3845-3852(1998).
EMBL; Y14026; CAA74355.1; -. HSSP; P06971; 1BY5.
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Last sequence update)
       of the FhuA proteins of Escherichia
                                                                                                                InterPro; IPR000531; TonB boxC. Pfam; PF00593; TonB_boxC; 1. Receptor. 732 AA; 80897 MW;
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
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                                                                                                                                                                                                                                       MEDLINE=1595285. PubMed=11759840;

A MEDLINE=1595285. PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sabamoto S.,

A Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yamada M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing

T. "Complete genomic sequence of the filamentous nitrogen-fixing

T. "Complete genomic sequence of the filamentous nitrogen-fixing

T. "Complete genomic sequence N.; Prockinio.";

I. DNA Res. 8:205-213(2001).

R. EMBL; APRO1588; BAB73335.1; -.

R. REL, APRO1588; BAB73335.1; -.

R. Pfam; PF00593; TonB boxC; 1.

R. Pfam; PF00593; TonB boxC; 1.

R. Receptor; Complete prockenme.

SEQUENCE 858 AA, 95042 MW; 93AA9B341C8C5003 CRC64;
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11.2%; Score 424; DB 16; Length 8:
Best Local Similarity 23.8%; Pred. No. 1e-16;
Matches 170; Conservative 124; Mismatches 328; Indels
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                              Anabaena sp. (strain PCC 7120).
Bacteria: Cyanobacteria; Nostocales; Nostocaceae;
NCBL_TaxID=103690;
                                Ferrichrome-iron receptor.
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Best Local :
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000531; TonB_boxC.
Pfam; PF00553; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN.
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                                                                                                                                                                                                                                                                                          HVFVG-ADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTP
      LDGRGVSPPLDTKNPTQGRPVDAIDF-
                                                     EQGRTTLYARGGLALNEFRSIPOVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPA
                                                                                                                                                                                                                                       DIFAGNEDENDSVQKQGRVGYEFEHRLNDTFVFRQNARVSTLNIDADWAFAYAP-----
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                                                                                                                                                                            AGRPGCNTADDKACAVGLGT-EIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTN
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(TrEMBLrel. 20, Last annotation
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Pred. No. 9e-17;
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Best Local
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                                                                                                                                                                                                                                                                                           Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8Z908;
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                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of a enterica serovar Typhi CT18."; Nature 413:848-852 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhi.
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01-MAR-2002
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                                                                                                                                                                   1 MFATTRMALLIGGAIGGATFPLFAQETTKNDTV
KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASFRPAEKNNRHE
                                                             YEYSEYN---IDGLP--AQMQSINGTLFNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR
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                                             FSDGSLDNVYLDGLKMMGDTNSHSSLVVDPWFLEDIEVVRGPASVLYGRSSPGGIVSLTS
                                                                                                        TRLATPDIETPQSVSIITRQQFEEQGATSVRQAVSYTPG--VYSNQIGASNRFDYIVLRG 101
                                                                                                                                   TKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSS----VYARG
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23.1%; Pred. No. 1e-16;
tive 121; Mismatches 3
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hia M.,
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Db 135 QDANTIRVSIVGETILPTAELFBSDEGLIFGLTSVTASLPPQQPETQSEQPSPAAEEPIE 194  Qy 46 AIVT-EKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLR 104  :	Db 254 GSTWAFIGNOITIRGESTSWLPILRDGFRIYENFSFQETSNLEEVLKGPASVQYG 310 Qy 163 SGEMGGIVNLVRKRPTKAFQCHAAAGEGTHKQYKAEADVSGSLNSDGSVRGRYMAQTYGA 222 Db 311 QLDPGGVINLVTKKPLSEPPYEIQAQFGSYGLIRPSFDVSGPLTDDGKLLYRLNA-TYQR 369	SPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSL	Db 427 PYSRVFNDPD-DFIDTKSFSIAYNLEHRFSDNWILKNSFKTLGQULFIGAILAGSLNEII 405 QY 333 KLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYN 392  L	Db 529 KGLLDDLVFRGTRTTLNIENPVYGVPPRTDFSTLPPATPFKNETTRLGFYLGDGTALNN- 587  Qy 417 RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFPPADGLSLIGGGRLGHYKIES 476  Db 588OFTILA	477 GEG 623	537 VGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTP	597 KWQIHAGYSYLHSQIKTASNSRDGGIFLLMPGH 	Qy 648 GVNAMSGITSSAGRHAGGYATFDAMAAYRFTFKLKLQINADALFNKHYAKV 959	ω .	RESOLI 38 P72609 ID P72609 PRELIMINARY; PRT; 853 AA. AC P72669;	ABLrel. 02, Cr ABLrel. 02, La ABLrel. 20, La receptor.	OS Synechocystis sp. (strain PCC 6803). OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis. OX NCBI TaxID:1148;	RN [1] RP SEQUENCE FROM N.A. RX MEDLINE=97061201; PubMed=8905231; RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto S., Kimura T., RA Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
		<u> </u>							<u> </u>			<u>.</u>	<del>.</del>
ERY POH SNT TPA	Db 273 FFEGEDDYDKYDRRENMYGYNIEHLFDNGWSVRQKLRYLHTKVTLNQVYAAGWLN 327 Qy 341 GRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQ 400	OY 401 GRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPA 458  Db 375 NHTTGYYGAFPPIDAFNPVYGAQPDYTLYSREKHKLRQTGYYLQDQM-SW 424  OY 459 DGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSKISQLY 514  OY 659 DGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSYGLYSGLY 514  OF 650 DGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSYGLYB 682	515 TPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTR 57 516 T	Db 540 YRSIGEIESKGVELEAISHLSDSVRLQAAYTYTDIRYKKSSPQEGGKRAVYAPRNQASAW 599 Qy 635 TTYQVTPELTIGGGVNAMSGITSS-AGMHA-GGYATFDAMAAYRFTPKLKLQ 684	Qy 685 INADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722     :  :        ::       ::     bb · 660 LNVNNLTDKRYVAACNSL-SYCYFGABRSIVGSVSWAF 696	RESULT 37 QBYUZ6 ID QBYUZ6 PRELIMINARY; PRT; 853 AA.			-0,2,3,5	Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada Yasuda M., Tabata S.;		DR FLEMI'S FOODS', CONDIDER POOSS', SEQUENCE 853 AA; 94548 MW, 67EA77C09E049437 CRC64;	Query Match 11.1%; Score 420.5; DB 16; Length 853; Best Local Similarity 23.1%; Pred. No. 1.6e-16; Matches 187; Conservative 117; Mismatches 327; Indels 177; Gaps 30; Qy 3 QFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYN 45

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ASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFE 536
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1201; PubMed=8905231;
110 S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
DYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLR
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00539; PYROKININ; UNKNOWN_1.
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Tabata S.
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DLNNSFQIPSYLRTDI---SVFYRRNNWRAAINVNNLFNIDYIBAT
                                                                                                              LAAYEITVSNLAVTDPENPNFS----IPSGEQRSKGVEFDIAGEILPGWNIIASYAYTDA
                                                                                                                                            VSFYRMKDKNAAA--PLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHS
                                                                                                                                                                                             GYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNAR
                          DAMAAYRFTPKLKLQINADNIFNR--HYYARVGGANTFNIPGSERT
                                                         RVTKDDNLEPGNLLEGVPFNSASLWSTYEIQ---
                                                                      NDFPDVFSSEGQTNTLG1FLQDQVTLTDNLKLLMGGRFDT1DQSSSSNGESDERYDQAFS
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akeuchi C., Wada T., Watanabe A., Yamada M.,
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                                                       ---AGDLQGLGFGLGLFYVGERQG
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MEDLINE=2195285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing
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Pfam; PF00593; TonB_boxC; 1.
Receptor; Complete proteome.
SEQUENCE 857 AA; 94906 MW;
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                                                   VGYKGSYMDDRLNARVSFYRMKDKNAAA---PLNPNNKKTRYAALGKRVMEGVETEISGAV
                                                                                                                                                                                                                                                                                                                              IGEFTVRNYELQTDLVGNFATGSIQHTLLFGVDLSWVNDGGVSL--FEPAPSIN-IFNPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVTGQQDRYSVFNATTATRTDTPLKDIPQSIQAVPRQVLEDRQVIRASDALRSVSGVQQG 263
VGVRGEFLNGSLITNLAAYEITRSNLAVTDPDNPNFS----IPSGEQRSRGVELDVTGQI
                                                                                                                                         GEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFE
                                                                                                                                                                                                                                                                                                                                                                                    LGN-TANEFVIGADYNRFRSTNEQGRTTLYA-----RGGLALNEFRSIPQVDLIANAR
                                                                                                                                                                                                                                                                                                                                                                                                                                             YSSSDQTNN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVAFGTG-IADIPFDRVLG-----EPDDFSERTNFLAGYRLEHRFNDDWKLRNQFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPADANNKLPSLPQHVFVGADWNKFKMNSHDVFAD-----LKHYFGNGGYGKVGMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGF--GTHKQYKAEADVSGSLNSDGSVR 212
                                                                                                                                                                                                                    YGT-----ATRPSRDEFADVFPFGSQTDSIGVFVQNQITLAENLKLLVGGRFDNIDQSS
                                                                                                                                                                                                                                                                          KGVRGYSHTVATENLDEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YRLNA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRVMAQTVGASPRPAEKNN---RHETFYAA--ADWDINPDTVLGAGYLYQQRHLAPYN-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPASVLYGNLDPGGVINFVTKQPLS--EPFYAAGLQVGSFGLVRPTLDLSGPLNPERTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKVGGTSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNDDGRSSVYARGYEYSEYNIDGLPAQMQSINGTLPNLF------AFDRVEVMR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 20,
(TrEMBLrel. 20,
(TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 415.5; DB 16; ilarity 23.6%; Pred. No. 3.2e-16; Conservative 106; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AYERGGNFRNFDTEVERFFISPVVTWKIGDRIDLRLELEY-SNDKRPYDRG
                                                                                                            FSPRVGIVYQPIEPISLYTSFSRSFQPNFGNRADGSLLEPVRGTQYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----FNIRGFP----OFGGNLRDGFNNRNNFSIVETANLERIEVLK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                             -RLEPGRLNETTGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7120).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7D4C98620AEB8007 CRC64;
                                                                                                                                                                                                                                                                          -GIYGKSTFHPADGLSLIGGGRLGHYKIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::| |:| |:| |: | ::| |: | 339
282 VEHQLGSGWKVDAGLSYRTSRLFGKSSDASRLLDDGRTLWRQARERD--YHANDLAGRVD 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 ITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA-RGY-----EYSEYNIDGLPAQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 VṛRAALDGFGATRLDTALDWVSGISRONNLGGIADNFAIRĠFAGDLNTGSDYLVNĠFSA- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 ALSSSYFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSVSI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                       ---YATFDAMAAYRFTPKLKLQINADNIFNRHYYA--- 697
                                                                                                                                                                              -DIVLGAGYLYQQRHL-APYNGLPADANNKLPSLPQHVFVGADWN---KFRMNSHDVFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Artiguenave F., Gouzy J., Mangenot S., Artiguenave F., Camtelloo L., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Welsenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Ature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OYKAEADVSGSLNSDGSVRGRVMAOTVGASPRPAEKNNRHETFYAAADWDINP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, beta subdivision, Ralstonia group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                              | | : | |:||:||:|
725 LPGWNLIASYAYTDARVTKDDNLQPGNLLDGVPFNSASLWSTYEIQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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Best Local Similarity 22.8%; Pred. No. 3.7e-16;
Matches 170; Conservative 127; Mismatches 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.9%; Score 412; DB 16; 22.8%; Pred. No. 3.7e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      689 AA
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01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
putative ferrichrome-iron receptor protein.
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InterPro; IPR000531; TonB boxC.
Pfam; PF00539; TonB boxC; 1.
Complete proteome:
SEQUENCE 689 AA; 74213 MW;
                                                                                                                                                                                                                                                                                               698 ----RVGGANTFNIPGS 710
                                                                                                                                                                                                                                                                                                                                                               836 ORRNRINPGEPFTVRGT 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSC2729 OR RS00125.
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                                                                                                                                                               655 ITSSAGMHAGG-
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08XVU8
1D CON WALD
DT 01-MAD
DT 01-MAD
DT 01-MAD
DT 01-JU
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OC RAISE
OC RAIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 -KIPASLREIPOSYSIITNOQVKDRNVDȚFDQLARKTPGL--RVLSNDDGRSSVYARGYE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barnett M.J., Fisher R.F., Gapela D., Galibert F., Gouzy J.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Guzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Kaeting D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            643 LTIGGG---VNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARV 699
                                                                                                                                                                                                                                                                                      587
                                                                                                                                                                                                                                                                                                                       588 TEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL-MPKHSANLWTTYQV----TPE 642
                                                                                                                                                                                                                                                                                                                                                                                                                              549 LDVSGQLTPNLKVLGTYAYTDARV-TADTVLPSGAPLSNIPRHSASALGLYEFGAGSLGR 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664
                                                                                                                               432
                                                                           471
12 MTAATVLAALSSSVFAAQ-----TADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 RSI-----PQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGH
                                                                                                                            385 DPVYGQPRPALRPSSSTRESORG-------FGAFVQDQVTLTPQWKLLAGVRMDR
                                                                                                                                                                                                                530 ROGNQFEVGYKGSYMDDRLINARVSFYRMKDKNAAA--PLINPNNKKTRYAALGKRVMEGVE
                                                                                                                                                                                472 YKIESGEGKTLHKAS--KTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pSymk (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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10.9%; Score 411; DB 16; Length 714;
Best Local Similarity 24.6%; Pred. No. 4.5e-16;
Matches 187; Conservative 110; Mismatches 344; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECLING BEGINE AND PRESENCE AURICALOUS OF LINE WILLIES SIDOTHIZODHUM MEALINE BSYMA MEGAPLABMIG.";
SIDOTHIZODHUM MEALINE ST. U.S.A. 98:9883-9888 (2001).
EMBL, AEO07282; AAK65621.1; -:
InterPro; IPRO00531; TonB boxC.
Pfam, PF00593; TonB boxC.
Peeptor; Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 714 AA; 78235 MW; 4DABSF4862934A69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative ferrichrome-iron receptor.
RA0963 OR SMA1747.
Rhizobium meliloti (Sinorhizobium meliloti)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665 --ASSYNELWVAPGAERQVTLAATYTF 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21396509; PubMed=11481432;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
STRAIN=1021;
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RESULT RESULT ID PERSON PORT OF THE PROPERTY O
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       Query
                                                                                                                                                                                            STRAIN=ZM4;
Shin I.S., Kang H.S.;
Shin I.S., Kang H.S.;
"Zymomonas mobilis ZM4 fosmid clone 43E12 complete sequence.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF300471; AAG42412.1; -.
HSSP; P06971; 1QJQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9EZ93;
Q9EZ93;
01-MAR-2001
01-MAR-2001
                                                                            Receptor.
                                                     SEQUENCE
                                                                                                                InterPro; IPR001899; Gram pos anchor.
InterPro; IPR000531; TonB boxC.
Pfam; PF00593; TonB boxC; 1.
PROSITE; PS00343; GRAM POS ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zymomonas mobilis.
Bacteria; Proteoba
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=542;
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       Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOLNVNNLFDEKHVASKDSGAVYYN-PG--RSILATLROSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVWGTYTLEGDGARGDMLFGLGARYTDAYYTSITNTTSSESA--VVFDAAFTYKIQENTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLWTTYQVTPELTIGG----GVNA-----MSGITSSAGMHAGGYATFDAMAAYRFTPKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria; alpha subdivision;
                                                     762
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(TrEMBLrel. 16, Last sequence up
(TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                   83046 MW;
  10.9%;
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  Score
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                                                   F489525A093B358E CRC64;
  410.5;
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                                                          Q8XVB1 PRELIMINAMI,
Q8XVB1,
Q8XVB1,
O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence up
O1-JUN-2002 (TrEMBLrel. 21, Last annotation
O1-JUN-2002 (TrEMBLrel. 21, Last annotation
O1-JUN-2002 (TrEMBLrel. 21, Last annotation
             Ralstonia solanacearum (P
Bacteria; Proteobacteria;
                                          protein.
RSC2920 OR RS00173.
   Ralstonia
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                                                                                                                                                                                                                                                                                                                                                                   NSRDD-GIFL-LMPKHSANLWTTYQVT----PELTIGGGVNAMS----GITSSAGMHAGGY
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                                                                                       Salanoubat M., Genin S., Attiguenave F., Gouzy J., Mangenot S., Arlat M., Brilault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Chandler M., Moisan A., Robert C., Saurin W., Schiex T., Siquier P., Thebault P., Whalen M., Wincker P., Levy M., Schiex T., Genome sequence of the plant pathogen Ralstonia solanacearum."; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "MRBL; AL646072; CAD16677.1; -.
InterPro; IPR00531; TonB_boxC.
Press Tone M. C., Canter M., Cant
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                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 801 AA; 87071 MW; S577D637FF9203EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
10.9%; Score 410; DB 16; Best Local Similarity 22.5%; Pred. No. 6e-16; Matches 188; Conservative 115; Mismatches 341;
                                                                    STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RLGHY---KIESGE-----
                                                 FROM N.A.
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443 NLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLND 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TVGTKIPASLREIPĢSVSIJTNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120
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  748
                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=65699;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Markhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Rlack S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; Krain of Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 PSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSG-KTEKTRSYTIDRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYSEYNIDGLPAQMQSING-----TLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL
689 ASLDKWPIAIPTPRQIASLWTDYRIRSGVLQGVGIGAGVRYVSPTAGAPDNALRVPGYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

10.8%; Score 407.5; DB 16; Length 635;
Best Local Similarity 24.4%; Pred. No. 6.1e-16;
Matches 158; Conservative 111; Mismatches 258; Indels 121;
                                                FDAMAAYRFTPKLKLOINADNIFNRHYYARVGGANTFNI PGSERTWTANLRYSF
                                                                            ll protein; Complete proteome.
635 AA; 70757 MW; C477F457C36C41D2 CRC64;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20222556; Pubmed=10761919;
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EMBL; AL162756; CAB84891.1; -.
                                                                                                                                                                                                                                                                                                                                               Hypothetical protein NMA1663.
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ID P7259
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Best Local Similarity
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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MEDILINE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Okumura

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome. SEQUENCE 863 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
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01-FEB-1997 (TrEMBLrel. 02,
01-MAR-2002 (TrEMBLrel. 20,
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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01-FEB-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSVATGIDTP---IMDTPFSAQVVSEEVIRSQQAITLEDVLTNVSSVTFGGTTGGRETIFG 265
                                                      GSKLGMKTPAGRPGCNT--ADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIG
                                                                                                                                                                          ANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFA
                                                                                                                                                                                                                                 QPLERFAYAPIVTYAITDDTDLSLAVEYINDTNPADFGLSSFGDGVAPVPRSRVINDPSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRGFGNQFS----DTVPILRDGFRLYGGFQGITEVSHLQQVEVLKGPSSILYGQIEPGGV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RITVTGNGTVPAAQVIPSSENLILSLTPPINTV--ESEEEIEIVATREEEAAVQEFFVPN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RINMTA-ATVLAA----LSSSVFAAQTADLETVHIKGQRSYNAIVT-EKNGDYSSF---- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEIYERRHR-----VRPNTGATHGVYAGS--CQGSRTVICLLLWSGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -RGY--EYSEYNIDGLPAQMQSIN-----GTLPNLFAFDRVEVMRGPSGLFDSSGEMGGI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171;
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- IALPTIVNGPTVTRFFADQDG------QQGSYSFYTNAVGKFSTGSVKHELLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%; Score 402; DB 1 22.2%; Pred. No. 2e-15; tive 127; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                   LEHRFNENWKLRNAFRYMSYNYDYNV----
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                          --AGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPG
                                                                                                                       KNIVAVSDPVNPLFLST----IGTQQSQGIELDIVGEILPGWKIIGNYSYINAKVIEDTD
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YTVGDYIIGNAAIFYQ-RDKYRVALNLRNFTNANYVRAVSGNQTGIEPG
                                                          PNFVDNRLFGI-PYNMANLWTTYEIQS-----GALQGLGFGIGFNYVGDRFGDLANT
                                                                                        SNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMH------
                                                                                                                                              DKNAAA--PLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQI--KTA
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Copyright (c) 1993 - 2002 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
ь	3776	100.0		21	AAB07697	A Neisseria mening
2	3592	95.1	691	21	AAB07698	A Neisseria mening
w	3244	85.9		21	AAY75566	Neisseria meningit
4	821.5	21.8		22	AAU33610	Pseudomonas aerugi
ហ	784	20.8		20	AAY38831	Neisseria meningit
o	784	20.8		20	AAY38834	Neisseria gonorrho
7	778	20.6		20	AAY38832	Neisseria meningit
80	765	20.3		21	AAY75565	Neisseria gonorrhe
9	737.5	19.5		22	AAU34539	E. coli cellular p
10	676.5	17.9		20	AAY38833	Neisseria gonorrho

New Neisseria meningitidis polypeptide useful for diagnosis of Neisseria infection and for development of vaccines against such infection -

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Human	3 ABP0675	4 2	1.	٠	195	42
Human	Н	2	13		195	
Nove.	2 ABG1786	2	45	٠	196	
Novel	N	2	77		205	9
Neiss	1 AAY7553	7 2	18	٠	205	
Neisseria meni	1 AAY7553	8 2	18	٠	213	
TonB	1 AAY8009	N	78			
Escherichia	N	N	39		222.5	
Escherichia	2 ABB5266	N	66		228	
Neisseria	0 AAY38830	N	2	6.2	235.5	
Pseudomona	2 AAU3358	N	82	٠	237.5	
Neisseria	N	N	65	•	241.5	
E. coli	2 AAY7291	N	73	7.2	273.5	
Adhesin.	7 AAR7536	_	6.0	٠	294.5	
Neisseria	2 AAB68918	N	700	8.1	307.5	
Escherichia col	2 ABB5289	N	7:		313.5	
Neisseria	2 AAB6892	N	6,0		316.5	
Neisseria	2 AAB6891	N	6		316.5	
Neisseria	2 AAB6891	N	7(	9.6	363	
Neisseria	2 AAB6892	N	7(	9.7	364.5	
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Neisseria	2 AAB68916	N	7(	٠	370	
Neisseria	1 AAY75	N	703		370	
	2 AAB6892	N	7(	•	371	
Escherich	2 ABB52	3 2	66	9.8	371	
Neisse	2 AAB6892	2 2	70		374.5	14
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Neisse	1 AAY75	2	78	10.5	.7	
Neisse	CC/IWW T	2	,	٠	٠	

## ALIGNMENTS

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RESULT 1
AAB07697
ID AAB0
                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
WPI; 2000-476062/41.
N-PSDB; AAA59216.
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                                                                                                                                                                                                                                                                                                                                         BASB053; Neisseria meningitidis infection; vaccine.
                                                                                                                                                                                                                                                                                                                                                                              A Neisseria meningitidis BASB053 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB07697;
                                                       Ruelle J;
                                                                                                                              15-JAN-1999;
28-JAN-1999;
                                                                                                                                                                                       10-JAN-2000; 2000WO-EP00137.
                                                                                                                                                                                                                            20-JUL-2000.
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                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                99GB-0000959.
99GB-0001903.
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AAB07698 standard; Protein; 691

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                                    The present sequence represents a Neisseria meningitidis BASB053 polypeptide. The BASB053 polypeptide, or an antibody immunospecific for PASB053 may be identified in a biological sample in order to diagnose a Neisseria meningitidis infection in an animal. The BASB053 polypeptides and polynucleotides may be used as vaccines, for generating an immunor response in an animal. A composition comprising at least one antibody immunospecific for BASB053 may be used to treat humans infected with Neisseria meningitidis.
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ive 0; Mismatches
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             Page 55-56; 92pp;
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RESULT 2 AAB07698

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The present sequence represents a Neisseria meningitidis BASB053 polypeptide, or an antibody immunospecific for BASB053 may be identified in a biological sample in order to diagnose a Neisseria meningitidis infection in an animal. The BASB053 polypeptides and polynuclectides may be used as vaccines, for generating an immune response in an animal. A composition comprising at least one antibody immunospecific for BASB053 may be used to treat humans infected with Neisseria meningitidis.
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                                                                                       meningitidis BASB053 polypeptide
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 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, represent novel Neisseria meningitis and N.
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                                                               THAGGYATFDAMAAYRFTPKLKLQINADNI FNRHYYARVGSESTFNI PGSERSLTANLRY
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Pred. No. 2.5e-286;
3; Mismatches 48;
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RESULT 4 AAU33610 4

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DGLPAQMQSI----NGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQG 183
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97GB-0023516.
97GB-0024190.
97GB-0024386.
97GB-0025158.
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27-NOV-1997;
10-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella premoitae, Pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen or homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part

of the printed specification, but was obtained in electronic format directly from MIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 LTPRETPQSITVVTRQNMDDFGLNNIDDVMRHTPGITVSAYDTDRNNYYARGFSINNFQY 219
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                                                                                                                                                                                                                                                                                                                                                                                   Trawick JD,
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                                                                           Pseudomonas aeruginosa cellular proliferation protein #54.
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                                                                                                   Antisense, prokaryotic cellular proliferation protein, antibiotic, antibacterial, drug design.
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AAU33610 standard; Protein; 815
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23-MAY-2000; 2000US-206648F.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578F.
27-NOV-2000; 2000US-253625F.
22-DEC-2000; 2000US-253931P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                                        21-MAR-2001; 2001WO-US09180
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen KL,
Xu HH;
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                                                                                                                                           Pseudomonas aeruginosa
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Best Local Similarity
Matches 217; Conserv
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N-PSDB; AAS51469
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Yamamoto RT,
                                                  14-FEB-2002
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treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
HAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWD
                                                                                                                      280 HVELGAGSWDNYRSELDVSGPLTESGNVRGRAVAAYQDKHSFMDHYERKTSVYYGILEFD
                                                                                                                                                                           INPDIVLGAGYLYQQRHL--APYNG-LPA-DANNKLPSLPQHVFVGADWNKFKMNSHDVF
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 379-380; 524pp; English.
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                                                                                                                              RAADNLSLILGGRYTRYRTGSYDSRTQGMTYVSANRFTPYTGIVFDLTGNLSLYGSYSSL
                                                                                                                                                            HPADGLSLIGGGRLGHYKIESGEGKT--LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQL
                                                                                                                                                                                                                                                            TAATDLIPGYWHADPRTHSASVSLIGKYRLFGREHDLIAGINGYKYAS-NKYGE-----
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 NTYYRAANQAKTHGWEIEVGGRITPEWQIQAGYSQSKTRDQDGSRLNPDSV----
                           KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA
                                                                                           YTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN--AAAPLNPNNK 571
                                                                                                                                                                                                                             GGLALNEFRSIPQVDLIANARKGVRGYSHTVA----TENLDEFGI-----YGKSTF
                                                                                                                                                                                                                                                                                          ACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYAR 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRLTRKPLFEVRAEAGNRKHFGLDADVSGSLNTEGTLRGRLVSTFGRGDSWRRRERSRDA 235
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                                                               FVPQSQKDEHGSYLKPVTGNNLEAGIKGEWLEGRLNASAAVYRARKNNLATAAGRDPSG-
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Pred. No. 4.5e-62;
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10-DEC-1997;
14-JAN-1998;
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06-NOV-1997;
14-NOV-1997;
                                                                                                                                                                                                                                      Amino acid sequences AAY38499-Y38944 represent Neisseria meningi and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for their fragments, their nucleic acids and antibodies are used for the fragments, prevention (as vaccines) or treatment of Neisseria diagnosis, prevention (as vaccines) or treatment of Neisseria
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                                                                                                                                                                                                                                                                                                                             Claim 4; Page 384; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                        diagnosis,
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SGTHTPFGLPMTLREIPQSVSVITSQQMRDQNIKTLDRALLQATGTSRQIYGSDRAGYNY 115
                                                                                 MSVFRIMMTAATVL-----AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSS 57
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                      FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQ-LARKTPGLRVLSNDD--GRSS 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Masignani
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97GB-0023516.
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                                                                                                            Score 784; DB 20;
Pred. No. 4.5e-62;
5; Mismatches 321;
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                                                                                                                                        Length 725;
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         SRNRALNIFAGIEHRFN-----QDWKLKAEYDYTRSR--FRQPYGVAGVLSIDH 341
                                                                                                                                                               STAATDLIPGYWHADPRTHSASMSLIGKYRLFGREHDLIAGINGYKYAS-NKYGERSIIP 400
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                                                                        ETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGADWNK 290
                                                                                   AELYGILEYDIAPQTRVHAGMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPATNWSN 294
                                                                                                            FKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADD 350
                                                                                                                                                  KACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYA 407
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                                                                                                                                                                                                                           FHPADGLSLIGGGRLGHYKIESGEGKT - - LHKASKTKFTGYAGAVYDLNDNNSLYLSLSQ 512
                                                                                                                                                                                                                                                                LYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN-AAAPLNPNNK 571
                                                                                                                                                                                                                                                                           KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA 631
                                                                                                                                                                                                                                                                                                                                         632 NLWITYOVTPEL----TIGGGV------NAMSGITSSAGMHAGGYAIFDA 671
                                                                                                                                                                                                                                             FRAADNLSLILGGRYSRYRAGSYNSRIQGMIYVSANRFIPYIGIVFDLIGNLSLYGSYSS 501
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treatment; Neisseria infection; meningitis; septicaemia; gonorrhea.
VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR
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KHPTRKPLFEVRAEAGNRKHFGLGADVSGSLNAEGTLRGRLVSTFGRGDSWRQLER-SRD
                                                                                                                                                                                                 RGGLALNEF------RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKST
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                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis strain A antigen encoded by ORF23.
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97GB-0024190.
97GB-0024386.
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Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRHRALNLFAGIEHRFN------QDWKLKAEYDYTRSR--FRQPYGVAGVLSIDH 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 NTAATDLIPGYWHADPRTHSASVSLIGKYRLFGREHDLIAGINGYKYAS-NKYGE---- 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQ-LARKTPGLRVLSNDD--GRSS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
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                                                                                                                                                                                   Proteins from Neisseria meningitidis and N. gonorrhoeae useful diagnosis, treatment and prevention of infection
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                                                      Scarlato V;
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                                                   Grandi G, Masignani
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CHIR-) CHIRON SPA
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 Best Loc
Matches
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                                                                      AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrhaee polynucleotides and polypeptides. AAZ54576 and AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                   Sequence
                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                       Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics -
                                                                                                                                                                                                                                                                                                                             WPI; 2000-062150/05.
N-PSDB; AAZ54327.
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02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY75565 standard; Protein; 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-1998;
25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1999;
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Local Similarity
les 143; Conserv
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INST GENOMIC RES.
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                                                                                                                                                                                                                                                                                     and diagnostics
                                                                                                                                                                                                                                                                                                                                                                              Galeotti C, Grandi G, Pizza M, Rappuoli R,
                                                   154
                                                                                                                                                                                                                                                                                                                                                                   Pizza M,
Venter J
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98US-0098994.
98US-0099062.
98US-0103749.
98US-0103794.
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99US-0121528
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            20.3%;
          Score 765; DB 2:
Pred. No. 2e-61;
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Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence
                       DB 21; Length 154;
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                                                                                                                                                                                                                                                                                                                                                                               Masignani V,
Scalato E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 2604
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Conservative

6

Mismatches

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The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CE Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence represents an CC use of the prokaryotic cellular proliferation protein.

CC of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-611495/70.
N-PSDB; AAS52398.
                                                                                                                                                                                                                                                                                        Example 3; Seq ID No 10132; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
23-OCT-2000;
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23-MAY-2000;
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2000US-206848P.

2000US-207727P.

2000US-242578P.

2000US-253625P.

2000US-257931P.
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Xu HH;
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us-09-889-267-2.rag

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treatment; Neisseria infection; meningitis; septicaemia; gonorrhea
                                                                                                                                                                                                          Pizza M,
                                                                                                                                                                                                                                                                                           Claim 4; Page 383; 524pp; English.
                                                                                                   98GB-0019016.
97GB-0023516.
97GB-0024190.
97GB-0025158.
97GB-0025157.
                                                                                 98WO-IB01665
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                     Neisseria gonorrhoeae
                                                                                                                                                                                                           Masignani
                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                               WPI; 1999-327407/27.
                                                                                                                                                                                       (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                          623 AA;
                                                                                                                                                                                                                                         P-PSDB; AAY38833.
                                        WO9924578-A2
                                                                                                                06-NOV-1997;
14-NOV-1997;
18-NOV-1997;
                                                                                 09-OCT-1998;
                                                             20-MAY-1999
                                                                                                     01-SEP-1998
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10-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STGTPIPGSNGETAYKAVDGTVSKGVEFELNGAITDNWQLTFGATRYI-----AEDNEG 620
                                                                                                                                               234
                                                                                                                                                                                                                                                             TFYAA-ADWDINPDTVLGAGYLYQQRHL--APYNGLPA-DANNKLPSLPQHVFVGADWNK 290
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                                                                                                                                                                                                                                                                                                                                                                 GFDYVGGTGWNSGKRKVDALDLFADGSYELFGRQHNLMFGGSYSKQNNRYFSSWANIFPD 422
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                                                                                                                                    VGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYE 121
                                                                                                        Gaps
                                                                                           OFMSVFRINMTAATV-LAALSSSVFAAQTADLETVHIKGORSYNAIVTEKNGDYSSFAVT
                                                                                                                                                                            YSEYNIDGLPAQMQS----INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT
                                                                                                                                                                                        SREFKGDVSAEYGSWNKERYVADLQSPLTEDGKIRARI----VGGYQNNDSWLDRYNSEK
                                                                                                                                                                                                                                                                          -KAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGA---SPRPAEKNNRHE
                                                                                                                                                                                                                                                                                                                 EF-GIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNN
                                                                                                                                                                                                                                                                                                     FKMNSHDVFADLKHYFGNGGYGKVCMRYSDRDADSNY----AFAGSKLGMKTP----
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                                                                        105;
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                                                    Length
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                                                   22;
                                                              Best Local Similarity ..... Mismatches 308; Matches 211; Conservative 148; Mismatches 308;
                                                   19.5%; Score 737.5; DB 2
27.3%; Pred. No. 7.8e-58;
format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                             Local Similarity
                               729 AA;
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                                Sequence
                                                    Query Match
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meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNRHETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SRDAELYGILEYDIAPQTRVHAGMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPAT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 TADDKACAVGL---GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRT 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKSTFHPADGLSLIGGGRLGHYKIESGEGKT--LHKASKTKFTGYAGAVYDLNDNNSLYL 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 GYNYLFARGSRIANYQINGIPVADALADTGNANTAAYERVEVVRGVAGLPDGTGEPSATV 69
                                                                                                                                                                                              Proteins from Neisseria meningitidis and N. gonorrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQ-TVGASPRPAEK
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                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequences AAV38499-Y38944 represent Neisseria meningit and N. gonorrhoeae antigenic proteins. They are encoded by open treading frames (ORFs) AAZ11972-Z1358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used diagnosis, prevention (as vaccines) or treatment of Neisseria infections, such as meningitis, septicaemia and gonorrhea. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.9%; Score 676.5; DB 20; Length 30.0%; Pred. No. 2.2e-52; tive 90; Mismatches 277; Indels
    Scarlato
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Rappuoli
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31-JUL-1998;
02-SEP-1998;
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Petersen J,
Tettelin H,
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09-OCT-1998;
09-OCT-1998;
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                   AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54576 and AAZ54576 and AAZ54713 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis
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                                                                                                                                                                                                                                                           Claim 2;
                                                                                                                                                                                                                                                                                                        Novel Neisserial polypeptides predicted vaccines and diagnostics -
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Best Local :
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                                                        AMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY----YARVGGANTFN
                                                                                    GYTYNKSRYKNAAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVS
                                                                                                               GYSYLHSQIKTAS---
                                                                                                                                          FALFYLEQKNRTVVDFGYVPGAGGKQGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFA
                                                                                                                                                                    VSFYRMKDKN-----AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHA
                                                                                                                                                                                                                                                                                  ADGLSLIGGGRLGHYKIESGEGKTL----KFTG
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                             AQSGTSSLYNIRQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFY
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                                                                                                                                                                                                                         YAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGK-LLKPRQGNQFEVGYKGSYMDDRLNAR
                                                                                                                                                                                                                                                       TGRLHLLGG--LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTP
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  722
                                                                                                              -NSRDD--GIFLLMPKHSANLWTTYQV-TPELTIGGGVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 400.5; DB 2
Pred. No. 4.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRPGCNTADDKACAVGLGTEIKQKALA----
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                                                                                                                                                                                                                                                                                                                                         -----STFHP
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the invention
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TTLYARGGLALNEFRSIPQ-----
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                                                                                                                                                                                                                                GRLGHYKI ESGEGKTL-
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                                                                                  RFRST----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N gonorrheae polynucleotides and polypeptides. AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseriab bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                             Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 YAAADWDINPDTVLGAGYLYQQ-------RHLAPYNGLPADANNKLPSLPQ 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKLGMKTPAGRPGCNTAD---DKACAVGLG-----TEIKQKALA------ 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGIAEADAGDSSVLTLGGMYOKSREVPDFSGIILSCENOKTAPFSSTP--ACNRPLOLPR 60
                                                                                                                                                                                                                                                                                                                                        Mora M;
Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 HVFVGADWNKFKMNSHDVFADLKHYFGNG-------GYGKVGMRY-----
                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Neisserial polypeptides predicted to be useful antigens for
                      Neisseria meningitidis ORF 742 protein sequence SEQ ID NO:2542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 220; Indels 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 783;
                                                                                                                                                                                                                                                                                                                                        Masignani V,
Scalato E, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.5%; Score 397.5; DB 2
21.3%; Pred. No. 8.6e-27;
ive 92; Mismatches 220
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                                                                                                                                                                                                                                                                                                                                        Hickey F
Ratti
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 1209; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                        Grandi G,
Rappuoli R,
                                                                                                                                                                                         98US-0083758.
98US-0094869.
98US-0098054.
98US-0103749.
98US-0103749.
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(first entry)
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, Pizza M,
                                                                                                                                                                                                                                                                                                                                                    Petersen J, Pizza M,
Tettelin H, Venter JC;
                                                                                              Neisseria meningitidis
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N-PSDB; AAZ54296.
                                                                                                                     WO9957280-A2
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|: : | | | : | | SRRAAERKAGFDECMSAPFALDFICQGSWGDPGVDADKSEFVDKALAKEGIFNNAAQRFP 240
                                                                                                                  241 NSLYDSSFNRKATANRRYSYMPLRHTKDDRQWGIKLDLTGTYGLFGREHDFFVGYAYGDE 300
                                                                                                                                                                                                                                          KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEPDGDLSSPLVRGHKEPDWQAYDEKGN 360
                                                                                                                                                                                                                                                                                                     433
                                                                                                                                                                                                                                                                                                                                    DNNSLYLSLSQLYTPQTNLDADGK-LLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDK 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------LGNTANEFVIGADY--N
                                                                                                                                                                                                                                                                                                     -----VDLIANARKGVR-----
                                                                                                                                                                                                                                                                                                                                                                                                          -----GYSHT-----VATENLDEFGIYGK------STFHPADGLSLIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-----AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660 GMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY----YARVGGANTFNIFGSERTWT
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                 ---FDASYSR------PFR-----
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Best Local Simi
Matches 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          against Neisseria infections e.g. bacteremia and meningitis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating
 660
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 LGWNH-KNVNVTFAAANLLNOKYW--
                                                                                                                                                                                   YGGRGYLSIDTSSAAVFNAAPEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNIRYRPDP
                                                                                                                                                                                                                                                                                                                                                                                                        CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
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                          AAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
                                                                                        MPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG-----
                                                                                                                       KNNPYIYAVSGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPDRVGIHLN
                                                                                                                                                    NNKKTRYAALGKRVMEGVETBISGAVTPKWQIHAGYSYLHSQIKTASNSRDD---
                                                                                                                                                                                                                  ----QTNLDADGKLL---KPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNP
                                                                                                                                                                                                                                                 KFVLGGRYDKYTFNSENKLT---GNSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP
                                                                                                                                                                                                                                                                                                               LGYRGSF-----TVP-INPYDRASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPDL
                                                                                                                                                                                                                                                                                                                                          LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
                                                                                                                                                                                                                                                                                                                                                                           QQT-----DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                         AHRNDFYKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEYSEYNI---DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
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Pred. No. 7.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 336;
                                                         -GVIGI
-RSDSMPGNPRGYTARVNYRF
                                                          -GKRYGYNSRNKEVTTL PGFARVDAM
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Best Local S
Matches 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, f feveral genes from Neisseria meningitidis. These include the dsbA, f fhuA, rni5, rth17, rth18, rth19, rth21 and tolC genes. These be used in the diagnosis and treatment of infection by the bacterium which can lead to meningitis and bacteraemia, and in vaccines to pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic polypeptides derived from Neisseria meningitidis nucleic acids that encode them, useful for diagnosing and vacagainst Neisseria infections e.g. bacteremia and meningitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 20B; 240pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-082916/10.
N-PSDB; AAF56461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-1999;
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VGADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection.
                                                                                                                                                                                         YANFKOSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVS
                                                                                                                                                                                                                                        RPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGAS
                                                                                                                                                                                                                                                                                              RGFQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSK 169
                                                                                                                                                                                                                                                                                                                                                   RGYEYSEYNI -- PGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
                                                                                 PSITVKLDN-----GLKWT-----
                                                                                                                                   PRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVF
                                                                                                                                                                                                                                                                                                                                                                                                           VTRNGQL---IKETPQTIDTL---NIKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFD--QLARKTPGLRVLSNDDGRSSVYA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity 22.5%; Pr
175; Conservative 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rth;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 374.5; DB 22.5%; Pred. No. 9e-25;
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                                                                                 -GOYTYDNVERTPDRSPTKSVYDRF-GLPYRMG
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The invention relates to a library of DNA fragments of Escherichia colistrain polymucleotides (ABABST7-ABAB812) and ABAB8533) and encoded proteins (ABB52459-ABB52919 and ABB52954-ABB52954) but a B2/D+A-. The polymucleotides have potential antiinflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                         PGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGR 402
                                         AWQQT------DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR-----EHRN 374
                                                                                                                                                                              --- QTINLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDK 560
                                                                                                                                                                                                      485 APYGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERF 539
                                                                                                                                                                                                                               NAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD 620
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F-AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNY 333
                                                                                                                                                                                                                                                                                                  meningitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli strains for the given strain comprises polynucleotides
                                                                          TTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPAD
                                                                                                                                                                                                                                                                                  ---GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG-------
                                                                                                                             GLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLY
                                                                                                                                                                                                                                                                                                                                                   GYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bscherichia coli, B2/D+A-; antiinflammatory; antibacterial immunosuppressive; extra-intestinal infection; phylogeny; systemic infection; non-diarrhoeal infection; septicaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli polypeptide SEQ ID NO 263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pyelonephritis, antibiotic resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                             663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A library of DNA fragments of phylogenic determination of a
                                                                                                                                                                                                                                                                                                                                                                                                                           ABB52462 standard; Protein;
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          compositions used to treat, palliate or prevent extra-intestinal E. coll infections. The polypeptides are useful for determining the phylogenic group of a given E. coll strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicement, appeneithitis and meningitis this is particularly advantageous as bacterial resistence is increasing with the more frequent use of broad spectrum antibiotics.
antibacterial and immunosuppressive activity as part of pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATSSSFGGGT------GQLDITGPIEGTQLAYRLTGEVQDEDYWRNFGKERSTFI 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-AADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSH 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381
                                                                                                                                                                                                                                                           ALSSSVFAA-----QTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASL
                                                                                                                                                                                                                                                                                  71 REIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDG--RSSVYARGYEYSEYNID
                                                                                                                                                                                                                                                                                                                                             GLPAQMQSINGTLPNLF--AFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAA
                                                                                                                                                                                                                                                                                                                                                                                                             G-SIMTNGLRIVUPRSFNAATERVEVLKGPASTLYGILDPGGLINVVTKRPEKTFHGSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 DVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RVTAYDATTGTLTRRVDATQGSTQRMHATRADL------QGNVDIAGFYNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQDALYLTDNWIAVAGIRYQYYTQYAGKGRPPNVNTDSRDEGWTPKLGLVYKLTPSVSLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 ANYSQTEMPQSSIASYIGDLPPESSNAYEVGAKFELFDG-ITADIALFDIHKRNVLYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGIFLLMPKHSANLWTTYQV-----TPELTIGGGVNAMS--GITSSAGMHAGGYATFDAM
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                                                                                                                                                                                                                            Indels 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 663;
                                                                                                                                                                                         9.8%; Score 371; DB 22;
llarity 22.1%; Pred. No. 1.7e-24;
Conservative 121; Mismatches 285;
                                                                                                                                                                                                           Similarity
                                                                                                                                                              663 AA;
                                                                                                                                                                                                                         Matches 171;
                                                                                                                                                                Sequence
                                                                                                                                                                                              Query Match
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standard; Protein; 703

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Best Local S
Matches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhaB, fhuB, rni5, rth17, rth18, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-082916/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Meningococcus; meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis protein
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                                                                                                                                                            NFKQSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS
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                        CNTADDKACAVGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
                                                                                                                                                                                                                                                                                                                                                       FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection.
                                                   AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
                                                                              ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
                                                                                                        ITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
                                                                                                                                 PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
                                                                                                                                                                                      TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
                                                                                                                                                                                                                   FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
                                                                                                                                                                                                                                           YEYSEYNI---DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                                                                                                                                                                                      VTRNGQL---IKETPOTIDTLNIOKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
                                                                                                                                                                                                                                                                                                 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
                                                                                                                                                                                                                                                                                                                            FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
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MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
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-DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR----
                                                                                                                                                                                                                                                                                                                                                                                 131;
                                                                                                                                                                                                                                                                                                                                                                                               Score 371; DB 22;
Pred. No. 1.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Length 703;
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EHRNPT
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RESULT 17
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09-OCT-1998;
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
                                                                                                    Petersen
Tettelin
                                                                     WPI; 2000-062150/05
N-PSDB; AAZ54330.
                                                                                                                                                                                                                                                                                                                                                        antigenic; diagnosis; immunc antibacterial; gene therapy.
                  Claim 2;
                                      Novel Neisserial polypeptides predicted vaccines and diagnostics
                                                                                                                        Fraser C,
                                                                                                                                             (CHIR )
                                                                                                                                                                                                                                                                        30-APR-1999;
                                                                                                                                                                                                                                                                                             11-NOV-1999
                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGYSRAFTA-----SIDPYDRASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-YARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYGGRGGYLSINTSSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRYRPDEQNDPYTWAVGGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPD
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                                                                                                                                             CHIRON CORP
                                                                                                    Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein;
                  Page 1238; 1453pp;
                                                                                                                      Galeotti C,
                                                                                                    Venter JC;
                                                                                                                                             GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                               Pizza M,
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98US-0103794.
98US-0103796.
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98US-0094869
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                                                                                                                                             RES.
                                                                                                                                                                                                                                                                                                                                                                  immunogenic; infection;
                                                                                                            Grandi G,
Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               703
                  English.
                                                                                                                                                                                                                                                                                                                                                                                                  protein sequence
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                                                                                                             Hickey E,
Ratti G,
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                                                  þe
                                                  useful
                                                                                                             Masignani V, Mora M;
Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                  meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:2610.
                                                  antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   703
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AAZ53015 to AAZ54536,

AAZ54577 to AAZ54615,

and

AAY74253

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AAY75941

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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent beers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing in the manufacture of medicaments for treating or preventing infection due to be used to Seserie de.g. meningitis and septicaemia), to detect the be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :: : | |::|:| |: EQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NFKQSRNIGTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-- 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR------VMAQTVGASPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  488 YGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYOIERFNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
                                                                                                                                                                                                                                                                                                              138;
                                                                                                                                                                                                                                                                             Length 703;
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                                                                                                                                                                                                                                                                           9.8%; Score 370; DB 21; 1
llarity 22.4%; Pred. No. 2.3e-24;
Conservative 130; Mismatches 334;
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Matches 174; Conserv
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The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhaB, fhuA, rniS, rthl7, rth18, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :: : | | |: : | | | : : | | | | EQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                            meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FHLALLPTLIIA - - SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN - - YDEAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 ITVKLDN-----GLKWT-----GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic polypeptides derived from Neisseria meningitidis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 703,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%; Score 370; DB 22; Length 70 ilarity 22.4%; Pred. No. 2.3e-24; Conservative 130; Mismatches 334; Indels
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
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                                                                                                             Neisseria meningitidis protein #15
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                 AAB68916 standard; Protein; 703
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                                                                                                                                                                                       Neisseria meningitidis.
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N-PSDB; AAF56456.
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Matches 174; Conserv
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                                                                                                                                            Meningococcus;
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      Novel Neisserial polypeptides predicted vaccines and diagnostics -
                                                                                                                                                         09-OCT-1998;
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31-JUL-1998;
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                                                                                                                                                                                                                                                                                                            Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                             Neisseria
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DB; AAZ54329.
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                                                                                                                           CHIRON
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                                                                                                                                                                                                                                                                                                                                 diagnosis; immunc
ial; gene therapy.
                                                                                         Galeotti C,
                                                                                                                GENOMIC RES.
                                                                     Venter
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                                                                                Pizza M,
                                                                                                                           CORP.
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99US-0121528
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98US-0098994
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                                                                                                                                                                                                                                                                                                                                            immunogenic; infection; meningitis; septicaemia;
                                                                              Grandi G,
Rappuoli R,
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                                                                               Hickey E,
Ratti G,
                 to be useful antigens
                                                                              Masignani V,
Scalato E, (
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Best Local S
Matches 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polymucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polymucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLPGF
                                                                                                                                            AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD--
                                                                                                                                                                                                                                                 KFVLGGRYDKYTFNSENKLT---GSSROYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP
                                                                                                                                                                                                                                                                                   SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYTP
                                                                                                                                                                                                                                                                                                                                                       LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
                                                                                                                                                                                                                                                                                                                                                                                                                            CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
   ATFDAMAAYRFTPKLKLQINADNI FNRHYYARVGGANTFNI PGSERTWTANLRYSF
                                                                                                           RYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPDR
                                                                                                                                                                               YGGRGGYLSIDTLSSAVFNAD-----PEYTROYETGVKSSWLDDRLSTTLSAYQIERFNI
                                                                                                                                                                                                                                                                                                                      L----GFSSAFSASINPYD---RASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPDL
                                                                                                                                                                                                                                                                                                                                                                                           QQT-----DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YEYSEYNI -- DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTRNGQL---IKETPOTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
                                                                         -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 1237; 1453pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                -QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 368; DB 21;
Pred. No. 3.5e-24;
0; Mismatches 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 138;
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655

ARVDAMLGWNH-KNVNVTFAAANLLNQKYW-----RSDSMPGNPRGYTARVNYRF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhaB, fhuA, rniS, rth10, rth10, rth10, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR------VMAQTVGASPR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fhuA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFKQSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITVKLDN-----GLKWT------GOYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.7%; Score 368; DB 22; Length 703; 22.4%; Pred. No. 3.5e-24; Active 130; Mismatches 334; Indels 138;
                                                                                                                                                                                                                    meningitis; bacteraemia; vaccine; dsbA; fhaB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                              ż
                                                                                                                                                                               Neisseria meningitidis protein #26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 26B; 240pp; English
                                                           AAB68927 standard; Protein; 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 130;
                                                                                                                                                                                                                                                                                                                                                                                                    99EP-0401764
                                                                                                                                                                                                                                                                                                                                                                                                                                           99EP-0401764
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nassif X, Tinsley C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-082916/10.
N-PSDB; AAF56467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           rth; tolC.
                                                                                                                                                                                                                         Meningococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 such infection
                                                                                                                                                                                                                                                                                                                        EP1069133-A1
                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-1999;
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                                                                                                                                        18-APR-2001
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Matches 174;
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The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dabh, fhab, fhub, rni5, rth17, rth18, rth19, rth20, rth21 and to1C genes. These can be used in the diagnosis and treatment of infection by the bacterium,
                                                                                                                                                          Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
| |- |- | : | | : | | : | ARRIDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 336
                                                                                                                                    461
                                                                                                                                                                                                                                                                                    -----QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
                                                                                                                                                                                                                                                                                                                                                                 563 AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-- 620
                                                                                                                                                                                                                                                                                                                                                                                                                                            999
                                                       CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
                                                                                          ---DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
                                                                                                                                LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
                                                                                                                                                                                                           SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYTP
                                                                                                                                                                                                                                   YGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI
                                                                                                                                                                                                                                                                                                                                                                                         -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------GY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                602 VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fhaB; fhuA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARVDAMLGWNH-KNVNVTFAAANLLNOKYW-----RSDSMPGNPRGYTARVNYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meningococcus; meningitis; bacteraemia; vaccine; dsbA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis protein #19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-0401764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nassif X, Tinsley C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-082916/10.
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BASB082; BASB083; BASB091; BASB092; BASB0101; infection; vaccine;
                           A Neisseria meningitidis BASB083 polypeptide
                                                                                          AAB18720;
                                                                                                                     AAB18720 standard;
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                                                                                                                                                                                                                                                                                                                                       KNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRD
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                                                                                                                                                                                                                                                                                       D---GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------
                                                                                                                                                                                                                                                                                                                                                                                  FAPYGGRGGYLSINTSSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FHLALLPTLIIA--SFPVAAADTODNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
                                                                                                                                                                                                                           -GYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
                                                                                                                                                                                                                                                           PDRVGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTL
                                                                                                                                                                                                                                                                                                                       FNIRYRPDEQNDPYTWAVGGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKEN
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                                                          (first
                                                                                                                     Protein;
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Pred. No. 3.9e-24
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gene therapy; upper respiratory tract infection; bacteremia; meningitis; invasive bacterial disease.
WO200055327-A2
                                                          Neisseria meningitidis
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07-MAR-2000; 12-MAR-1999; 21-APR-1999 2000WO-EP01955 99GB-0005815 99GB-0009094

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23-APR-1999; 28-APR-1999; 07-MAY-1999; 99GB-0009503. 99GB-0009787. 99GB-0010710

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS

Defrenne Ç Delmelle Ç Ruelle J;

N-PSDB; AAA75745. 2000-602119/57.

Novel polypeptides designated BASB 082, 083, 091, 092, and 101 derived from meningococcus bacterium useful for producing vaccines against infections and in diagnostic assays -

Claim 3; Page 102-104; 108pp; English.

The present sequence represents a BASB083 polypeptide. The specification describes BASB082, BASB083, BASB091, BASB092, and BASB0101 polypeptides. The polymucleotides and polypeptides are useful as diagnostic reagents and for diagnosing N. meningitidis infection. The polymucleotides may be used as hybridisation probe for RNA, CDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding BASB082, BASB083, BASB091, BASB092 or BASB101 polypeptides and to isolate cDNA and genomic clones of other genes that have a high identity particularly high sequence identity to BASB082, BASB093, BASB091, BASB092 or BASB082, BASB093, BASB091, BASB092, BASB093, BASB091, BASB092 or BASB082, BASB083, BASB091, BASB082, BASB093, BASB091, BASB092 or BASB082, BASB083, BASB091, BASB083, BASB091, BASB093, bacteremia and meningitis.

Sequence 703 AA;

Ş 밁 δ 멹 Ś 밁 Ş 밁 á S Query Match Best Local Similarity Matches 172; Conserv 286 233 178 117 120 61 60 Ŋ α YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177 FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA ADWNKFKWNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG ITVKLDN------GLKWT-------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG NFKQSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR------VMAQTVGASPR 225 FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG VTVGTKIPASLREIPOSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA Conservative 133; 9.7%; Score 366; DB 21; Pred. No. 5.4e-24; 33; Mismatches 333; Length Indels 138; Gaps 116 119 60 59 344 276 285 232 33

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which can lead to meningitis and bacteraemia, and in vaccines
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                                                                 Similarity
                                702 AA;
             such infection.
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                                                                             Matches 177;
                                 Sequence
                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhab, fhuA, rni5, rth17, rth18, rth19, rth20, rth21 and tol6 genes. These can be used in the diagnosis and treatment of infection by the bacterium,
                                                      377
                                                                             461
                                                                                          L----GFRRNFTASIDPYD---RASRPASGRLQRILAQDRHKADSYGIFVQNIFSATPDL 430
                                                                                                                          516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
| | | : | | : | | : | AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 336
                                                                                                                                                487
                                                                                                                                                                      562
                                                                                                                                                                                                                  AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-- 620
                                                                                                                                                                                                                                 -GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------GY 666
                                                                                                                                                                                                                                                                                602 VGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYNSRNKEVTTLDGF 654
                                CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT 404
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                                               -----DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
                                                                                                                                                                     -----QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA
                                                                                                                          SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GAVYDLNDNNSLYLSLSQLYTP
                                                                                                                                       488 YGGRGGYLSINTSSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI
                                                                              LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
                                                                                                                                                                                                                                                                                                                         | | | | | : | : | | | | | | | ARVDAMLGWNH-KNVNVTFAAANLFNQKYW-----RSDSMPGNPRGYTARVNYRF 703
                                                                                                                                                                                                                                                                                                             ATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 meningitis; bacteraemia; vaccine; dsbA; fhaB;
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis protein #21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meningococcus;
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                                                                                                                                                                                                                                                                                                                                                                                                                  AAB68922;
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to prevent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVWRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: :| ||: |-::|| |: 17 FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 NFKQSRNIGAVYGWANR-SLNMDINEVLNKOVAIRLIGEVGRANSFRSGIDSKNVMVSPS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | | : |||: || AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L-YARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGYNRAFSA----SINPYD---RASWPASGRLQPILTQNRHKADSYGIFVQNIFSATPD 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYT 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486 PYGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYOIERFN 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GIFLLMPKH-SANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG------G, 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600 RVGIHLNNTSNVTGNLFFRY--TPTENLYGEI----GVTGT-GKRYGYDSRNKEVTTLPG 652
                                                                                                                                                                                                                                                                                                                                                                            FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITVKLDN-----GLKWT-----GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 QQT------DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-----QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 AAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD-
                                                                                                                                                                                                                                                            Indels 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666 YATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
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                                                                                                                                                                              Length 702;
                                                                                                                                                                                  DB 22;
                                                                                                                                                                              9.7%; Score 364.5; DB 22;
larity 22.8%; Pred. No. 7.3e-24;
Conservative 129; Mismatches 330;
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rni5; rth; tolC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhab, fhub, rnis, rth17, rth28, rth18, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Fig 18B; 240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection.
               SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYTP
                                                                                                                                       CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA 59
                                                                          LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
                                                                                                                                                                                                ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG
                                                                                                                                                                                                                                ITVKLDN-----GLKWT------GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
                                                                                                                                                                                                                                                           PAEKNNRHETFYAAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPOHVFVG
                                                                                                                                                                                                                                                                                          NFKQSRNIGAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPS
                                                                                                                                                                                                                                                                                                                                                        FQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRTNGGGVINMVSKYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                   VTRNGQL---IKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRG-ESIFLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
                                              L----GFSSAFSASINPYD---RASWPASGRLQPILTQNRHKADAYGIFVQNIFSATPDL
                                                                                                                                                                     AHRNDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW
                                                                                                                                                                                                                                                                                                                          TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR 225
                                                                                                                                                                                                                                                                                                                                                                                     YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     703 AA;
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                                                                                                        ----DNKTLSSNLTLNGDYTIGRFENHLTVGMDYSR----EHRNPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 363; DB 2
Pred. No. 1e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
Length 703;
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RESULT 25
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                                                           Query Match
Best Local S
Matches 142
                                                                                                                                                                     The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhab, fhub, rni5, rth17, rth18, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                               Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
                                                                                                                                                         such infection.
                                                                                                                                                                                                                                                                   Claim 3; Fig 16B; 240pp; English.
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N-PSDB; AAF56457.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (INRM ) INSERM INST NAT SANTE & RECH MEDICALE (PLAC ) MAX PLANCK GBS FOERDERUNG WISSENSCHAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYRPDEQNDPYTWAVGGKHRSRGVELSAIGQIIPK-KLYLRGSLGVMQAKVVEDKENPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP
FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA
                            FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
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                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein;
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                                                                                                                          697 AA;
                                                             Conservative
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                                                                        8.4%;
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                                                        %; Score 316.5; DB 2
%; Pred. No. 1.7e-19;
107; Mismatches 286
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                                                                                                                                                                                                                        KFVLGGRYDKYTFNSENKLT---GSSRQYSGHSFSPNIGAVWNINPVHTLYASYNKGFAP 487
                                                                                                                                                                                                                                                                                             :|| ::|||: :|||| YGGRGGYLSIDTLSSAVFNAD-----PEYTRQYETGVKSSWLDDRLSTTLSAYQIERFNI 542
                                 YEYSEYNI -- DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                      PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
                                                                                                                                        ADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPG 344
                                                                                                                                                          AHRNDFVKDKLOVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNYAW 336
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                                                                                                                                                                                                                                                                                  ------QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
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VTVGTKI PASLREI PQSVSI I TNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG
                                                                    TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR-----GR-----VMAQTVGASPR
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                                                                                                                       ITVKLDN------GLKWT------GOYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF-
                                                                                                                                                                            CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTT
                                                                                                                                                                                                                                               SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYTP
                                                                                                                                                                                                             LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATEN---LDEFGIYGKSTFHPADGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic polypeptides derived from Neisseria meningitidis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meningococcus; meningitis; bacteraemia; vaccine; dsbA; fhaB;
                                                                                                                                                                                                                                                                                                                     AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGY 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE. (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhaB, fhuA, rniS, rthl7, rth19, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent
nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEYSEYNI -- DGLPAOMOSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: :| ||::|:| ||: EQADASDIYRDGVRESGQ-VRRSTANI---ERVEILKGPSSVLYGRINGGGVINMVSKYA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 ITVKLDN-----GLKWT-----GQÝTÝDNVERTÞDRSPTKSVYDRF-GLÞYRMGF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   462 SLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA----GAVYDLNDNNSLYLSLSQLYTP
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                                                                                                                                                                                                                                                                                                                                                                               Indels 107;
                                                                                                                                                                                                                                                                                                                                   Length 697;
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                                                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                              8.4%; Score 316.5; DB 22;
llarity 22.1%; Pred. No. 1.7e-19;
Conservative 107; Mismatches 286;
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                                                                      Claim 3; Fig 24B; 240pp; English
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B2/D+A- The polynucleotides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, paliate or prevent extra-intestinal E. coli infections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  advantageous as bacter frequent use of broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a library of DNA fragments of Escherichia colistrains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A library of DNA fragments of phylogenic determination of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAR-2000; 2000FR-0003145
02-FEB-2001; 2001FR-0001449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia;
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                                                                                        LRKKLVSVALDWNIQPGTQLQLDASHYEFIQKGYVGSFNYGP---NVKLPSAPNPKDKNL
                                                                                                                     NRHETFYAAADWDINPDTVL---GAGYLY-QQRHLAPYNGLPADANNKLPSLP----QHV
                                                                                                                                                                                   NLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKN
                                                                                                                                                                                                                                                                             LGTKSWIETPYSSTTVTKEMIENQQAQSVSEMLKYSPSTQMQARGGMDVGRPQ--SRGMQ 118
                                                                                                                                                                                                                                                                                                                                                                        RINMTAATVLAALSSSV----FAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT
GSKLGMKTPAG--RPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIG
                             ALSTAGN--DLTTDTISTRLIHYFNDDWSMNAG---VGWQQADRAMRSVSSKILNNQGDI
                                                           FVGADWNKFKMNSHDVFADLKHYFG----NGGYGKVGMRYSDRDADS-----
                                                                                                                                                    NFVAKRPTEETLRKVTLGYQSRSAFTGHADLGGHFDENKRFGYRVNLLDQEGEGNVDDST
                                                                                                                                                                                                                     GSVVANSRLDGLNIVSTTAFPVEM---
                                                                                                                                                                                                                                                YS---EYNIDGL-----PAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV 170
                                                                                                                                                                                                                                                                                                          KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSN---DDGRSSVYARGYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spectrum antibiotics.
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The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fh. fhuh, rni5, rth17, rth18, rth19, rth20, rth21 and tolC genes. These c. be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent

prevent

can

Sequence

700 AA

infection.

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RESULT :
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                                                                                                               Immunogenic polypeptides derived from Neisseria meningitidis and nucleic acids that encode them, useful for diagnosing and vaccina against Neisseria infections e.g. bacteremia and meningitis -
                                                                                              Claim 3;
                                                                                                                                                              N-PSDB;
                                                                                                                                                                                             Nassif X,
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                                                                                                                                                                                                                                                                                               17-JAN-2001.
                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis
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(PLAC ) MAX PLANCK
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                                                                                                                                                       YEYSEYNI--DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRP 177
                                                                                                                                                                                                        TKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVR----GR-----VMAQTVGASPR 225
                                                                                                                                                                                                                                                         PAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG 285
                                                                                                                                                                                                                                                                                 233 ITVKLDN-----GLKWT-----GQYTYDNVERTPDRSPTKSVYDRF-GLPYRMGF- 276
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                           Gaps
                                                                          5 FHLALLPTLIIA--SFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYIN--YDEAA 60
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is His, this differs from Seq ID5, residue
is Gly"
                                                   FRINMTAATVLAALSSSVFAAQTAD-----LETVHIKGQRSYNAIVTEKNGDYSSFA
                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adhesin; plasmid pear; vector; vaccine; intestine colonisation.
 Length 700;
Query Match 8.1%; Score 307.5; DB 22; Length Best Local Similarity 21.9%; Pred. No. 1.1e-18; Matches 138; Conservative 109; Mismatches 285; Indels
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98 ILIDGVRQGGSSDVTPNGFSAMNTGFMPLAAIERIEVIRGPMSTLYGSDAMGGVVNIIT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 RKNADKWLSSVNAGLNLQESNKWGNSSÖFNFWSSGPLVDDSVSLOVRGSTOOROGSSVTS 217
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                                                                                                                                                                                                                                                                                                                                                  A candidate adhesin (AAR75366) was identified that is a homologue of the IrgA protein of Vibrio cholerae. The adhesin enables Escherichia coli O157:H7, an antibiotic-resistant, virulent and common food-borne pathogen, to adhere to epithalial cells. Recombinant adhesin was obtd. by expression of the encoding sequence (see AR10105) in E. coli HB101 (pax7). The adhesin can be used as a vaccine for immunisation of cattle against disease or colonisation of mucosal surfaces by O157:H7, thus increasing the safety of food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 RINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPA 68
                                                                                                                                                                                                                                                epithelial adhesin -
a vaccine to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 KLTNAAASVSVISQEELQSSQYHDLAEALRSVEGVDVESGTGKTGGLEISIRGMPASYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRPTKAFQGHAAAG-----FGTHKQYK----AEADVSGSLNSDGSVRGR-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 LPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%; Score 294.5; DB 17; Length 696; ilarity 20.7%; Pred. No. 1.7e-17; Conservative 103; Mismatches 302; Indels 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RITTLASVVIPCLGFS--ASSIAAABDVMIVSASGY----EK-
                                                                                                                                                                                                                                              Chromosomal DNA from E. coli 0157:H7 encoding isolated on plasmid pSC (overlap), for use as bacterial colonisation of bovine intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 31-32; 42pp; English
                                                                                 CHILDREN'S HOSPITAL & MEDI
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UNIV WASHINGTON STATE RES
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              95WO-US06994
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Matches 172; Conserv
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              07-JUN-1995;
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           The invention relates to the identification of iroNec gene, from an extraintestinal isolate of Escherichia coli. This gene is expressed in increased amounts in human urine and is identified by transposon (TnphoA) mutagenesis. iroNec gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY72914 standard;
                                                                                                      Novel isolated iroNec polynucleotide from extraintestinal isolate Escherichia coli useful as vaccine for treating or preventing extraintestinal infections caused by extraintestinal pathogenic
                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. coli iroNec
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                                                                     Page 39-41; 44pp;
                                                                                                                                                                                         Carlino
                                                                                              COLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising nucleotide sequence encoding one or more antigenic epitope of iroNec is useful for diagnostic and immunotherapeutic purposes. The iroNec antigenic peptide is useful for treating or preventing extraintestinal infections (EIs) caused by extraintestinal pathogenic E. coli (ExPEC). The EIs include urinary tract infection (UTI), meningitis, intra-abdominal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGRV------MAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLG--AGYLYQQRH
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                              SAGMHAGGYATFDAMAAYRFTPKLKLQINADNI FNRHYYARVGGANTFNI PGSERTWTAN
                                                                PLSVIPKYTINNSLNWTITQAFSASFNWTLYGRQKPRTHAETRSEDT
                                                                                               FL-LMPKHSAN------LWTTY-----QVTPELTIGGGVNAMSGITS
                                                                                                                             TASGAYILKWQNGGKALVDGIEASMSFPLVKERLNWNTNATW-----MITSEQKDTGN
                                                                                                                                                                 TRYAAL----
                                                                                                                                                                                                                              LYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKK
                                                                                                                                                                                                                                                                                                                                                            ANARKGVRGYSHTVATENLDEF-GIYGKSTFHPADGLSLIGGGR-------
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-SGKELGAYSLVGTNFNYDINKNLRLNVGVSNILNKQIFRSSEGANTYNEPG--RAYYAG
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                                                                                                                                                             -GKRVMEGVETEISGAVTPK---WQIHAGYSYLHSQIKTASNSRDDGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of several genes from Neisseria meningitidis. These include the dsbA, fhaB, fhuA, rni5, rth17, rth18, rth19, rth20, rth21 and tolC genes. These can be used in the diagnosis and treatment of infection by the bacterium, which can lead to meningitis and bacteraemia, and in vaccines to prevent such infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic polypeptides derived from Neisseria meningitidis and the nucleic acids that encode them, useful for diagnosing and vaccinating against Neisseria infections e.g. bacteremia and meningitis -
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                                                                                                                                                                                                                                                                                                                                                            Meningococcus; meningitis; bacteraemia; vaccine; dsbA; fhaB; fhuA;
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                                                                                                        RESULT 31
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
                                              P-----NDFVKDKLQVWRSDLEYAFNDKWRAQWQLAHRTAAQDFDHFYAGSEN 326
                                                                                                                                                                                327 GSRIKRNYAWQQT------DNKTLSSNFTLNGDYTIGRFENHLTVGMDYSR- 371
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PSLPQHVFVGADWNKFKMNSHDVF-ADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKL 334
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2000US-207727P.
2000US-242578P.
2000US-253625P.
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Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGASYDAHGDRIAPEPSQGDLFDSN---VYNIGGKLGLRIDENQRVQLALSHYDARQDTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVPLNTNRDSGRNLANIDPALIERIEVIRGSSAIY-GSGATGGIIS-ITTRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP-ASLREIPQ-S
                                                                                                                                                                                                  SNLEPVKTNNYELGWRGAIGGNTLGSLALFYTTSKLGDVQSFNNGLILTR----TKERIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAADWDINPDTVL---GAGYLYQQRHLAPYN----GLPADANN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSLAT-----EYGQTLRGRSMLVMVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSE-----YNID 128
                                                                                                                                                                                                                                                    KLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVME 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPFRLGNTAN-EFVIGADYNRFRS---TNEQGRTTLYARGGLALNEFRSIPQVDLIANAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSNYAFAGSKLGMK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YATDPRVARLPPGSVPANAIKGLELDE-QNRIRNTLANLEY----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGFGTHKQYKAEADVSGS-----LNSDGSVRG---RVMAQTVGASPRPAEKNNRHETFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLPAQM-QSINGTLPNL--FAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHA 185
  NNRLQATFFDSKDY--
                                               NSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAY
                                                                                              GVEASADWLSDDEVWGAGGSATWMRGREKPDGKDWQDMTGYRVPPLKLTAYLQYKPDADW
                                                                                                                                                     GVE---
                                                                                                                                                                                                                                                                                                                                                  ESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLS------QLYTPQTNLDADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRTPLGESGNTELVWGGDYNQERSDMPLDVFDPAAYDASGGLVFDKIGKLTYMPPLRTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -ENLDILGSRLSAQLYYRDYFTRFTPFDARAVSTRG-----GNVDQIMQNSEVFGSRLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGG----ENRAETRLSATSPLTRLGSDG-LGGQFQQYFAGSLGALDYSFDFGTRH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAVPATQARSEPLDMEQMEITASRTSSDLVS-----ATRQSTVIEHAQLEELRQGS
                                                                                                                                                                                                                                                                                                                                                                                                       AGAFAQLQHRFDEHWSIDGGLRYEYSTAEFDDFIPLSES----KAASPVTVKGGDLDYDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KLP--SLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                813 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.3%;
                                                                                                                                                                                                                                                                                                 ---LGIVYSPVAGQEIYASFSQGFQLPDVGIQLRNARRGFDIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -RGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKI 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107;
                                                                                                                                                TEISGAVTP---KWQIHAGY-----SYLHSQIKTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 237.5;
Pred. No. 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 301;
-----RLDGVESFGRRQVSTYTTVDLVSQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253;
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                                                                                                                                                        Matches
                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                  infections, such as meningitis, septicaemia and gonorrhea. Bo organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                      and N. gonorrhoeae antigenic proteins. They are encoded by open reading frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for diagnosis, prevention (as vaccines) or treatment of Neisseria
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 379; 524pp; English
                                                                                                                                                                                                                                                                                                                                                                              diagnosis, treatment and prevention
                                                                                                                                                                                                                                                                                                                                                                                Proteins from Neisseria meningitidis and diagnosis, treatment and prevention of ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-1997
14-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1998;
                                                                                                                                                                                                                                                                                                                           Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ12258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1997
10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY38830 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-1998
                                                                                                                              111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR-) CHIRON SPA.
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121
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                        231 NRHETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGAD 287
                                                  61
                                                                                                                                                                     Local Similarity
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SRXAELYGILEYDIAPQTRVHAXMDYQQAKETADAPLSYAVYDSQGYATAFGPKDNPATN
                                                                          NLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKN 230
                                                                                                    GYNYLFARGSRIANYQINGIPVADALADTGNANTAAYERVEVVRGVAGLLDGTGEPSATV
                                                                                                                             GRSSVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFTPKLKLQINADNIFNRHYYARV-----GGANTFNIPGSERTWTANLRYSF 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RITPDDQLSLGIQNLFNRDYYPLYSQLLRNNNNTSHLPAPGTVLTASYTHNW
                                                                                                                                                      64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria infection; meningitis; septicaemia; gonorrhea.
                                                                                                                                                                                                           211 AA;
                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98GB-0019016.
97GB-0023516.
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98GB-0000759
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                                                                                                                                                                   6.2%;
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                                                                                                                                                      34; Mismatches
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                                                                                                                                                                   Score 235.5; DB Pred. No. 6.2e-13
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                                                                                                                                                                                  211;
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                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a library of DNA fragments of Escherichia colistrains comprising polynucleotides (ABA8877-ABA88729 and ABA89533) and encoded proteains (ABB52919-ABB52914-ABB53094) of nature B2/D+A-. The polynucleotides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, pallate or prevent extra-intestinal E. coliinfections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advancageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides of
                                                                                                                                                                                    Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; pyelonephritis; antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 YEYSE--YNIDGLPAQMQS--INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV---- 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSS---VYARG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------EAPMMVSVIDTSAPENQTATSATDLLRHVPGITL--DGTGRTNGQDVNMRG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.0%; Score 228; DB 22; Length 660; Best Local Similarity 19.7%; Pred. No. 1.8e-11; Matches 157; Conservative 107; Mismatches 276; Indels 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                Tinsley
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                                                                                                                                                                                                                                                                                                                                                                                        (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                              Escherichia coli polypeptide SEQ ID NO 732.
                                                                                                                                                                                                                                                                                                                                                                                                               Clermont O,
                                                                                     ABB52669 standard; Protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Fig 6; 646pp; English.
              WNKFKMNSH----DVFADLKHYF 306
                                                                                                                                                                                                                                                                                                                            12-MAR-2001; 2001WO-EP03445.
                                                                                                                                                                                                                                                                                                                                                    2000FR-0003145
2001FR-0001449
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                Bonacorsi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-550253/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  660 AA;
                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phylogenic deter
nature B2/D+ A-
                                                                                                                                                                                                                                                                          WO200166572-A2
                                                                                                                                                                                                                                                                                                                                                   10-MAR-2000;
02-FEB-2001;
                                                                                                                                      11-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                 Bingen E,
                                                                                                              ABB52669;
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288
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94 YDHRGVLVLVDGVRQGTDTGHLNGTFLDPALIKRVEIVRGPSALLYGSGALGGVISYDTV 153
                                                                            ---NLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSV-----RGRVMAQTVG 221
                                                                                                                                                 154 DAKDLLQEGOSSGFRVFGTGGTGDHSLGLGASAFGRTENLDGIVAWSSRDRGDLRQSNGE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 WDRSTIQRDAQLSYKLAPQ----GNDW------LNADAKIY-----WSEVRINAQN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 TANEFVIGADYNRFRSTNEQGRTTLYARGGLALNE-----FRSIPQVDLIANAR-KG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: | :| | : | | | : : | | | - : : : - - SHLLTYGGEYYR-QEQATTGFPQAKIDFSSGWLQDEITLRDLP-ITLLGGTRYDS 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 GYA------GAVYDLNDNNSLYLSLSQLYT----PQTNLDADGKLLKPRQGNQFEVGY 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 KGSYMD----DRLNARVSFYRMKDKN------AAAPLN---PNNKKTRYAALGKRV 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPE 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 MIKYTTDL------SSLDVAYN-----RTRGKDTDTGEXI------SSINPD 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTIGGGVN---AMSGIT-----SSAGMHAGGYATFDAMAAYRFTPKLK--- 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; phylorephritis; antibiotic resistance.
                                                                                                                                                                                                                                  222 ASPRPAEKNNRHETFYAAADWDI--------NPDTVLGAGYLYQQRH
                                                                                                                                                                                                                                                                                                          214 TAPNDESINN----MLAKGTWQIDSAQSLSGLVRYYNNDAREPKNPQTVEASD----SSNP
                                                                                                                                                                                                                                                                                                                                                                                       LAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 RDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 TGSSGEYREQITK------GARLENRSTLFADSFA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 GLRFDDLMLSNDALEFKASYFDTKAKDYISTTVDFAAATTMSYNVPNAK----IWGWDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli polypeptide SEQ ID NO 1077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ż
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAR-2000; 2000FR-0003145.
02-PEB-2001; 2001FR-0001449.
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627 TTLVLGNAFDKEYWSPQG
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a library of DNA fragments of Escherichia coli strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature B2/D+A-. The polynucleotides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. coli infections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat in undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicemia, pyelonephritis and meninglitis this is particularly advantageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nature B2/D+ A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                DVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTP-AGRPGCNTADDKACAV 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASVSVITSEQLOKKPVSDLVDAVKDVEGISITGGNE-KPDISIRGLSGDYTLILVDG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIP 74
SFYRMKDKNAAAPLNPNNKKT-----RYAALGKRVMEGVETEISGAVTPKWQIHAGYS
                                     GIAKAFRAPSIREVSPGFGTLTQGGASIMYGNRDLKPETSVTEEIGIIYS-NDSGFSASA
                                                                                                               NEYAATDSLALTGGLRLDNHEI--
                                                                                                                                                                                                                              RSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATE--NLDEFGIYGK 452
                                                                                                                                                                                                                                                                   NAQGEILHPEIAVYQEKVIREVKSGKKDKYNHWDLNYESRKPEITNT----IIDAKVTAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTWDGVLGLGGIIQEHGKF-----GNSTTNDFYLSGPLIKDKLGLQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RRQSGRESRPNGSGGFEAGFIPPVEAIERIEVIRGPMSSLYGSDAIGGVINIITK-PVNN
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                                                                                                                                                                                          LPEN-----TTETQSVSIKQKAVFIE
                                                                                                                                                                                                                                                                                                                                           -VFE-----YGKNINOVHTLTPGESLDAWT-MRGNLKOPNSKRETHNSRSHWVAAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                            YAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSH
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                                                                           SLSQLY-TPQTNLDADG-----
                                                                                                                                                    STFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAG----AVYDLNDNNSLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQGHAAAGFG----THKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETF 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159;
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                                                                                                                                                                                                                                                                                                         -----KOKALAFDASY-SRPFRLGNTANEFVIGADYNRF 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SANTE & RECH
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                                                                         ---KLLKPRQGNQFEVGYKGSYMDDRLNARV
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                                                                                                                 --YGSYWNPRLYAVYNLTDNLTLKG
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              molecules can degrade or transport fumonisin and can reduce the pathogenicity of a fungus producing fumonisin. The plants may be e.g. maize, sorghum, wheat, tomato, soybean, alfalfa, sunflower, Brassica, cotton or rice. The products can also be used as detection reagents for fumonisins and related compounds. AAS91253 represents the Bacterium 2412.1 fumonisin catabolic gene cluster, and AAS91254 to AAS91273 represent isolated nucleic acids from Bacterium 2412.1 which encode AAY80085 to AAY80104. AAZ91286 to AAS91291 represent sequence used in the exemplification of the present invention. AAZ91274 to AAZ91285 are given in the sequence listing from the present specification but are not specifically mentioned further.
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters from a Bacterium 2412.1 fumonisin catabolic gene cluster. The Bacterium 2412.1 was isolated from maize. The nucleic acid molecules can be used for producing an enzyme for detoxifying fumonisin or a structurally related mycotoxin, e.g. in harvested grain, or processed grain which is to be used as animal feed or silage. Ruminal microorganisms transformed with the nucleic acid molecules can be used as probiotic compositions or as feed inoculant compositions. Plants transformed with the nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecules which encode fumonisin degradative enzymes and transporters, used for detoxifying fumonisin or related mycotoxin or reducing the pathogenicity of fungi producing fumonisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ91265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      374 RPFRLGNTANEFVIGADYNRFRSTNEQGRTTLY---ARGGLAL----NEFRSIPQVDLIA 426
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                                                                                                                                                                                                                                                                                                                  -----NSDGSVRGR 214
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                                                                                                     9 RINMTAATVLAALSSSVFA-AQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
                                                                                                                                    29 RLMLTAAGSALVLGLAPKALAQVAVPPAGHEASQEVQEIVVTAQ------RRS 75
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                               Length 785,
                               Query Match 5.8%; Score 220; DB 21; Length 76
Best Local Similarity 20.3%; Pred. No. 1.3e-10;
Matches 162; Conservative 109; Mismatches 345; Indels
                                                                                                                                                                                                                                                                                                                     168 GIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSL--
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AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria abacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used in gene therapy protocols.
Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
antibacterial; gene therapy.
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Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics
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27.7%; Pred. No. 5.8e-11;
tive 42; Mismatches 75;
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Rappuoli R,
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98US-0098894.
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Best Local Similarity 27.74
Matches 51; Conservative
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Tettelin H, Venter JC;
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                                                          Neisseria meningitidis
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09-OCT-1998;
09-OCT-1998;
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                                                                                                                                          30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                       Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                 Novel Neisserial polypeptides predicted vaccines and diagnostics -
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RMSTATGMR IAGKDTPQSVSVITRSRLDDKAVHTLEEAMKNTTGVNVVRDSGLQTRFLSR
                      AVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYAR 118
                                                                 FRINMTAATVLAALSSS------VFAAQTADLETVHIKGQRSYNAIV--TEKNGDYSSF
                                                 FSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGS---HALLGKTEKTRSYTID 62
                                                                                                                  Similarity
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INST GENOMIC RES
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                                                                                                                                                                                                                                                                                                                                                                       Page 1211; 1453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis; Neisseria gonorrheae; antigen; vaccine;
; diagnosis; immunogenic; infection; meningitis; septi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitidis ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Galeotti C, Grandi G, Pizza M, Rappuoli R,
                                                                                                                                                         187 AA;
                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0094869.
98US-0098994.
98US-0099062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy
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99US-0121528
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98US-0103794.
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                                                                                                                  5.4%;
27.6%;
                                                                                                      43;
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                                                                                                                  Score 205; DB 21;
Pred. No. 3.1e-10;
                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                              useful antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masignani V, Mora M;
Scalato E, Scarselli
                                                                                                                               Length 187;
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    septicaemia;
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                                                                                                    Gaps
122
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RESULT 39
AAU29336
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                                                                                                                                                               Matches
                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                  The invention relates to a method of identifying compounds that modulate a newly identified mar regulated (NIME) polypeptide activity. The method comprises contacting an NIME polypeptide with a test compound under interaction conditions, determining the ability of the compound to modulate the activity or expression of the polypeptide, and selecting the modulators. NIME nucleic acids and polypeptides are used in the treatment of microbial infections, and in screening for modulators of NIME expression and activity. These modulators can be used to reduce the infectivity of a microbe on a surface, and the virulence of a microbe in a subject suffering from an infection. AAU29379 represent Escherichia coli NIME amino acid sequences of the invention.
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 184-187; 526pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying compounds that modulate a newly identified mar regulated polypeptide activity, useful as antimicrobial compounds, involves contacting the polypeptide with a test compound -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS46238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Levy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mar regulated polypeptide; NIMR; microbial infection; antibacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĠFYIDQIGEDĠMTVNVAGRSĠYTAKIDVSPSTDĹAVYDHIÉVVRĠATĠĹTQŚNSEPĠĠTV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GYEYSEYNIDGLPAQMQSING---
             IITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYN------ID 128
                                           VESGLQQLLDGSGLQVKPLGNNSWTLEPAPAPKEDALTVVGDWLGDARENDVFEHAGARD 138
                                                                                                                                  LAALSSSVFAAQ-----
                                                                                                                                                               170;
                                                                                                      LAGLSFSAFAAQVNIAPGSLDKALNQYAAHSGFTLSVDASLTRGKQS-NGL----HGDYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUFTS COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barbosa TM,
                                                                                                                                                                                                                         774 AA;
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                             5.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alekshun
                                                                                                                                                                 108;
                                                                                                                                   -----TADLETVHIKGQRSYNAIVTEKNGDY- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NIMR) #8
                                                                                                                                                              Score 205; DB 2
Pred. No. 3e-09;
8; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV 170
                                                                                                                                                               316;
                                                                                                                                                                                           22;
                                                                                                                                                                                           Length
                                                                          GTKIPASLREIPQSVS 78
                                                                                                                                                               Indels
                                                                                                                                                               250;
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                                                                                                                                                                                                     SDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKOKALAFDASYSRPFRL 378
                                                                                                                                                                                                                                                                                               494
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SYLHSQIKTASNSRDDGIFLLMPKHSANL------WTTYQVTPELTIGGGVNAMSGIT 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSAGMHAG---GYATFDAMAAYRFTPK---LKLQINADNIFNRHYYARVGGANTFNI-PG 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VIRREDFAKTGATTMREVLNRIPGVSAPENNGTGSHDLAMNFGIRGLNPRLASRSTVLMD 198
                                                                                                             -------FYA---AADWDIN-----PDTVLGAGYLYQQRH-----LAPYNG---L 267
                                  GGTADNGFGTALLYSGTRGSDWREHSATRIDDLMLKSKYAPDEVHTFNSLLQYYDGEADM
                                                                                                                                                                       439 VATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGK----TLHKASKTKFTGYA
                                                                                                                                                                                                                                                                                                                                                                                                     GLPA------QMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA
                                                                FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHET----
                                                                                                                                                          PA-----DANNKLPSLPQHVFVGADWNKFKMNS--HDVFADLKHYFGNGGYGKVGMRY
                                                                                                                                                                                                                    GNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHT
                                                                                                                                                                                                                                                                                                                    ----YLDDKIDIGNWITTP-----GMRFEH--IESYQNNAITGTHEEVSYNAPLPAL
                                                                                                                                                                                                                                                                                                                                           GAVYDLNDNNSLYL----SLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNA
                                                                                                                                                                                                                                                                                                                                                                                        RVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEIS---GAVTP---KWQIHAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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139
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IQKVPQSISVVTABEMALHQPKSVKEALSYTPGVSV--GTRGASNTYDHLIIRGFAAEGQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQNNY-LNGLKLQGNFYNDAVIDPYMLERAEIMRGPVSVLYGKSNPGGLLNMVSKRPTTE 231
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                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KAFQGHAAAGFGTHKQYKAEADVSGSLNSDG--SVRGRVMAQTVGASP-----
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                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 48219; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to isolated
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                                                                                                         Tang YT;
23-AUG-2000; 2000US-0649167.
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nes 74; Conservat
                                                                                                            ပဲ
                                                                                                                                                               WPI; 2001-639362/73
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                                                      (HYSE-) HYSEQ INC
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                                                                                                                                                                                           N-PSDB; AAS82047.
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Human; open reading frame; ORFX; detection;

cytostatic; hepatotropic; nootropic; neuroprotective;

vulnerary; antipsoriatic; antiparkinsonian;

Human ORFX ORF673 polypeptide sequence SEQ ID NO:1346

anticonvolsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antixheumatic; antithyroid; antiviral; energy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

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                                                                                                                                                                                                                 cc antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; cc immunostimulant; cardiant; thrombolytic; cosqulant; vasotropic; cc antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; cc antidiabetic; hypotensive; dermatological; immunosuppressive; cc antidiabetic; hypotensive; dermatological; antifungal; antirheumatic; cc antidiamatory; antibacterial; antiviral; antifungal; antirheumatic; cc antidiamatory; and antianaemic. The sequences can be used for determining cc pathological conditions associated with an OREX-associated disorder. The cmucleic acids can be used to express OREX proteins in gene therapy cectors. The proteins and nucleic acids may be used to treat cancers, cc proliferative disorders, neurodegenerative disorders, osteoarthritis, cc profiferative disorders, neurodegenerative disorders, osteoarthritis, cc proteins on hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, alterias and naterias anaemia hurns woulds browner disorders, asthma, alterias anaemia hurns woulds browner disorders.
                                                                                                                                 Sequence
                                                                                                                                                                 allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 1152; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602362/57.
457 PADGLSLIGGGRLGHYKIESGEGKT-LHKASKTK--
                                                                            Similarity
                                                                                                                                 134
                                                            Conservative
                                                                             39
                                                                             .0%;
                                                       20;
                                                                            Score 195; DB 21;
Pred. No. 1.5e-09;
                                                            Mismatches
                                                          38;
                      ---FTGYAGAVYDLNDNNS 505
                                                                                             Length 134;
                                                          Indels 14;
 frame
                                                          Gaps
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bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis,

reperfusion injury in various tissues and conditions systemic cytokine damage.

for this patent did not form part of the printed

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RESULT 42
ABP06756
ID ABP06
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                                                           The present invention describes substantially purified human proteins CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated CC disorder in humans, and in the manufacture of a medicament for treating a gravine sociated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in the the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic contains a protein and treatment of disease, various immune deficiencies and disorders, infectious disease, autoimmune disorders such as multiple sclerosis, rheumatoid contricts, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, proteins are also and disease, and for gut
                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID 13494; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000;
29-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; open reading frame; ORFX; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX protein sequence SEQ ID NO:13494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP06756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmune disorder; rheumatoid arthritis; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperproliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mmune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYTSYTKIYKPQNSKDADRKLLDPIEGDTYEAGLKAAFFDGRLNASFAAFRIEQDNVA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTDDLSVILGTRVSNF---SGTDNTDFYDPTKADNRLTYRQTGVVTPYAGIVYDLNDIWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABN22508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RA, Leach MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-206132P
2000US-228716P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Å
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31-MAR-1999; 02-APR-1999; 05-APR-1999;

99US-0127607. 99US-0127636. 99US-0127728.

31-MAR-2000;

2000WO-US08621

WO200058473-A2 Homo sapiens.

Shimkets RA,

Leach

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(CURA-)

CURAGEN CORP.

2000US-0540763

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AAY34494;
                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
                                                                                       Query Match
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                                                                                                                                                               26
                                                                                                                                                                                                                                        646
                                                                                                              Matches
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specification, but was obtained in electronic format directly from WIPO
                                                                                                              -----FTGYAGAVYDLNDNNS 505
                                                                                       Gaps
                                                                                                                             . | | . . . | | | . | | | | | | | | . | . | | | | . . . | | | | . . . | . . | . . | . . . | . . . . . . . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                     i, chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                               506 LYLSLSQLYTPQTNLDADGKLLKPROGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAA
                                                                                    14;
                                                              Length 134;
                                                                                      38; Indels
                                                             5.2%; Score 195; DB 23; 39.0%; Pred. No. 1.5e-09;
             ftp.wipo.int/pub/published_pct_sequences.
                                                                                      20; Mismatches
                                                                                                              PADGLSLIGGGRLGHYKIESGEGKT-LHKASKTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID No 60111; 103pp; English.
                                                                                                                                                                                                                                                                                                                              Novel human diagnostic protein #29743.
                                                                                                                                                                                                                                                   ABG29752 standard; Protein; 340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0540217
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                      46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
                                                              Query Match
Best Local Similarity
                                     134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS93939
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001
                                                                                                                                                                                                                                                                             ABG29752;
                                     Sequence
                                                                                                              457
                                                                                                                                                                                                                                                                                                                                                                   food
                                                                                       Matches
                                                                                                                                                                                                                             RESULT 43
               at
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diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                528 KPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVE 587
                                                                                                                                                                                                                                                          588 TEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL--MPKHSANLWTTYQVTPELTI 645
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      702
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SDGANNETYGFHVDGA 200
                                                                                                                                                                                       Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                                    GGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 monas gingivalis; PG; periodontal disease; gingivitis; antigenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patterson MA;
                                                                                                                                               Length 340;
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                                                                                                                                                                                           69
                                                                                                                                             5.2%; Score 195; DB 22;
27.1%; Pred. No. 6.6e-09;
ative 26; Mismatches 69;
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Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98AU-0002911.
98AU-0003128.
98AU-0003338.
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97AU-0001182.
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98AU-0004917
                                                                                                                                                                                         Conservative
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Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-385613/32
                                                                                                                                                                   Local Similarity
Hes 48; Conserv
                                                                                                        340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX91712
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29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-AUG-1999
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RESULT 45
AAY34368
ID AAY3
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AC AAY3
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DT 25-1
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DE POIE
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KW POIE
KW VACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     especially gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity with a vaccine mechanism of action. The PG polypeptides can used as vaccines especially against Porphorymonas gingivalis. Probes be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                           AAY34368 standard;
vaccine; antigenic
                                              Porphorymonas gingivalis protein PG35
                                                                             25-AUG-1999
                Porphorymonas gingivalis; PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPQVDLIANARKGVRGYSHTVATENLDEFG----IYGK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THKOYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETVHIK--GORSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVD
                                                                                                                                                                                                                                                                                                                   NPNNKKTRYAALGK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKGFDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFSGGKDFFSLYASAQDVQRRSYYGGGDYTENLLNGAVQSGSTESDEYNDAFTALTSYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTK--AFQGHAAAGFG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLSQGLKFQPGLRVEDNCQNCGFNQVRINGLEGAYSQILIDSHPIFSSLAGVYGLEQMPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFDQLARKTPGLRVLSN--DDGRSSVYARGYE--YSE------YNIDGLPA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKVHIEKGGSRHVDLYLTEEILSLDGVVVS-ANRNETFRRQAPSLVTVLSPELFLKTNST 146
                                                                                                                                                                                                                     TIYNDKDG----VSKVYGVNLEGRIAYNKSFDLQLGG
                                                                                                                                                                                                                                                    TASNSRDDGIFLLMPKHSANL -- WTTYQVTPELTIGG
                                                                                                                                                                                                                                                                                    SPNLKEERSRSISASFDYYHRADEWQFNIMGEAFSTFISNQFKPSDKVETTSDGKEWIIR
                                                                                                                                                                                                                                                                                                                                                  PRANV-----RYNPNKNLSFRLSYSEGFRAPQYFDEDLHVELA------GGTPISRVL
                                                                                                                                                                                                                                                                                                                                                                              PQTNLDADGKLLKPRQGNQFEVGYK-----GSYMDDRLNARVSFYRMKDKNAAAP----L
                                                                                                                                                                                                                                                                                                                                                                                                                 DQL--
                                                                                                                                                                                                                                                                                                                                                                                                                                            DGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYD---LNDNNSLYLSLSQLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSRP---FRIGHTANE----FVIGADY--NRFRSTNEQGRTTL--YARGGLALNEFRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSKATLEYHSM---QEYRRGGDRLD-----NPPFEAQIAEYLQHYINGGSFKFDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GV-MVFGQHNYRPGQDIDGDNFTELPNLRNRSL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NM------IERVEVIRGGGSALFGSNAVGGVINVITKEPLRNSAEISHSTMTFD 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         833 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --QGGGMYRHTFG-ENWDFTGGLEYIYGQLDDRSGYRPSKIDQNTSTFSQY
                                                                                                                                                                                                                                                                                                                                                                                                                 --EYKTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GSFQNTTQFNGSMLTE-----DRKA
                                                                                                                                        Protein;
                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1%; Score 193.5; DB 20; 20.4%; Pred. No. 3.7e-08; tive 82; Mismatches 266;
                                                                                                                                                                                                                                                                                                                   -----RVM-EGVETEISGAVTPKWQIHAGYSYLHSQIK
                                                                                                                                           876
                periodontal
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             disease; gingivitis;
                                                                                                                                                                                                                       660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 207;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX94318 to AAX94583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX91586.
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22-MAY-1998;
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23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                   assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic Porphorymonas gingivalis peptides
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 365
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                                                                                                   HAKGW-----GSFQNTTQFNGSMLTE------
                                                                                                                          THKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVL
                                                                                                                                                                                                       NLSQGLKFQPGLRVEDNCQNCGFNQVRINGLEGAYSQILIDSHPIFSSLAGVYGLEQMPA
                                                                                                                                                                                                                                                                                   ETVHIK--GORSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPOSVSIITNOOVKDRNVD
YSKATLEYHSM---QEYRRGGDRLD--
                         YGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDA
                                                                          GAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGG
                                                                                                                                                        NM-----IERVEVIRGGGSALFGSNAVGGVINVITKEFLRNSAEISHSTMTFD
                                                                                                                                                                               QMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTK--AFQGHAAAGFG
                                                                                                                                                                                                                                  TFDQLARKTPGLRVLSN--DDGRSSVYARGYE--YSE-----YNIDGLPA 132
                                                                                                                                                                                                                                                            EKVHIEKGGSRHVDLYLTEEILSLDGVVVS-ANRNETFRRQAPSLVTVLSPELFLKTNST 189
                                                 GV-MVFGQHNYRPGQDIDGDNFTELPNLRNRSI
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                        gingivitis
                                                                                                                                                                                                                                                                                                                                                                876 AA;
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                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330-331;
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98AU-0003338.
98AU-0003654.
98AU-0004917.
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98AU-0002911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97AU-0001182
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                                                                                                                                                                                                                                                                                                                       5.1%; Score 193.5; DB 20.4%; Pred. No. 4e-08;
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Webb EA;
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                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DM,
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 -NPPFEAQIAEYLQHYINGGSFKFDQ
                                                                                                                                                                                                                                                                                                                                        DB
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                                                                                                                                                                                                                                                                                                              266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing
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                                                                                                                                                                                                                                                                                                              Indels 207;
                                                                                                                                                                                                                                                                                                                                      Length
                                                   -GFRSYYKTGL
                                                                                                                                                                                                                                                                                                                                         876;
                                                                                                     -DRKA
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                                                   364
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Search completed: December 18, 2002, 06:40:21 Job time : 53.9653 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Qy 9 RINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPA 	Query Match 7.9%; Score 296.5; DB 1; Length 6 Best Local Similarity 21.3%; Pred. No. 1.1e-18; Matches 176; Conservative 103; Mismatches 304; Indels	CHARACTERISTICS: 696 amino acids amino acid Y: linear TYPE: protein	REFERENCE/DOCKET NUMBER: CHOR-1-10286 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 1-206-682-8100;.1-206-224-0718 (direct) ; TELEPAX: 1-206-224-0779 ; INFORMATION FOR SEQ ID NO: 5:	/265,714 4 97	; APPLICATION NUMBER: US/08/765,081 ; FILING DATE: March 26, 1997 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: PCT/US95/06994 ; FILING DATE: June 7, 1995	MEDIUM COMPUTE OPERATI SOFTWAR CURRENT A	ton 7 FORM:	NUMBER OF CORRESPONI ADDRESS STREET:	ESULT 1  IS-08-765-081-5  Sequence 5, Application US/08765081  Patent No. 5798260  GENERAL INFORMATION:  APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary in the control of invention:  TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial	ALIGNMENTS	908 4 US-08-778-570B-22 908 4 US-09-059-584-22 908 1 US-08-487-890A-94 908 2 US-08-478-435-94 908 2 US-08-337-483-94 908 2 US-08-478-373-94 908 2 US-08-478-373-94 908 3 US-08-474-671-94 908 3 US-08-483-577A-94	172 4.6 915 3 US-08-483-577A-96 172 4.6 915 4 US-08-897-438-96 172 4.6 915 4 US-08-637-654-96 172 4.6 915 4 US-08-649-518-96 172 4.6 915 4 US-08-649-518-96 171 4.5 909 2 US-08-63-124A-4 169.5 4.5 908 3 US-08-613-009A-16	172 4.6 915 2 US-08-337-483-96 172 4.6 915 2 US-08-478-373-96 172 4.6 915 3 US-08-474-671-96
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98 ILIDGVRQGGSSDVTPNGFSAMNTGFMPDAAIERIEVIRGPMSTLYGSDAMGGVVNIIT 157
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                                                                                                                                                                                            KRPTKAFQGHAAAG------FGTHKQYK----AEADVSGSLNSDGSVRGR-----V 215
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SLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLS--NDDGRSSVYARGY--EYSE 124
                                                                                            --PAOMOSIN-GTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
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                                -----GESHLVTVGG----EFQSSSMKDGVVLASTG--
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Sequence S. Application US/09098082
Patent NO. 6040421
GENERAL INFORMATION:
APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | | | : : | | | 653 YSDVSLYSAGKSTLYAGDYFQTGSSTTGYVIP--ERNYWMSLNYQF 696
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage COMPUTER: IBM PC compatible/Pentium II OPERATING SYSTEM: MS-Windows 95
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STATE: WE
COUNTRY:
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98 ILIDGVRQGGSSDVTPNGFSAMNTGFMPLAAIERIEVIRGPMSTLYGSDAMGGVVNIIT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 696;
                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct) TELEFAX: 1-206-224-0779 INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%; Score 296.5; DB 3; ilarity 21.3%; Pred. No. 1.1e-18; Conservative 103; Mismatches 304;
                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/765,081
FILING DATE: March 26, 1997
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Sheines, Diana K.
REGISTRATION NUMBER: GAGS TO TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,082
FILING DATE:
Word for Windows-6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
TYPE: amino acid
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Matches 176; Conserva
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PCT-US95-06994-5
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                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US95-06994-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application PC/TUS9506994 GENERAL INFORMATION:
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                               Matches 176;
                                                                                                                                                                                                                                                                                                                          TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 696 amino acids
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CHOR-18591
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: BESSER, THOWAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL ADHESIN
NUMBER OF SEQUENCES: 14
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ZIP: WA 98101
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BRODERICK, THO REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/06994 FILING DATE: 07-JUN-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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KLTNAAASVSVISQEELQSSQYHDLAEALRSVEGVDVESGTGKTGGLEISIRGMPASYTL
                                 SLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLS--NDDGRSSVYARGY--EYSE 124
                                                                            RITTLASVVIPCLGFS-
                                                                                                        RINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPA 68
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University of Washington
Washington State University Research Foundation
TARR, PHILLIP I
                                                                                                                                             Conservative
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                                                                                                                                           7.9%; Score 296.5; DB 5 21.3%; Pred. No. 1.1e-18; tive 103; Mismatches 304
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Sequence 8, Application
GENERAL INFORMATION:
APPLICANT: Children
APPLICANT: Univers:
APPLICANT: Washing
APPLICANT: TARR, P
APPLICANT: TARR, P
APPLICANT: BILGE
APPLICANT: TARR, P
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ZIF: WA JULLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  APPLICANT: BILGE, SIMA S
APPLICANT: BESSER, THOMAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7
                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                  STATE: W
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                                                                                     ZIP: WA 98101
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                                                                                                                                           CITY:
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                                                                                                                                         SEATTLE
                                                                                                                                                                                                                                                                                                                                                                                                   Application PC/TUS9506994
                                                                                                                        WASHINGTON
                                                                                                                                                          SUITE 2800,
                                                                                                                                                                                                                                                                                                          Children's Hospital & Medical Center
University of Washington
Washington State University Research
TARR, PHILLIP I
                                                                                                        USA
                                                                                                                                                                              CHRISTENSEN, O'CONNOR, JOHNSON AND
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                                                                                                                                                              1420 FIFTH AVENUE
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RESULT 5
US-09-668-113A-8
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US-09-668-113A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.6%; Score 286; DB 5; Length 703; Best Local Similarity 20.4%; Pred. No. 1.1e-17; Matches 171; Conservative 104; Mismatches 304; Indels 258;
                                                                                                                                                                                                                                                                                                     Protein
E. coli O157:H7 adhesin amino acid sequence,
wherein "Xaa" residues represent gaps
introduced to facilitate best alignment with
SEQ ID NO:9.
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994 FILING DATE: 07-JUN-95 CLASSIFICATION: PRIOR APPLICATION NUMBER: US 08/265,714 APPLICATION NUMBER: US 08/265,714
                                                                                           APPLICATION NUMBER: US 08/265,714
FILING DATE: 24-JUN-1994
ATTORNEY, ACBNT INFORMATION:
NAME: BRODERICK, THOMAS F
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: CHOR-18591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
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STRAIN: 86-24 NALR
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MOLECULE TYPE:
DESCRIPTION:
DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                           -----NAMSGITSSA----GMHAGGYATFDAMAAYRFTPKLKL 683
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                                                                                                                            KPEESVSYEAGV---YYDNPAGLNANVTGFMTDFSNKIXVSYSINDNTNSYVNSGKARLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Russo, Thomas A.
TITLE OF INVENTION: Identification of A Vaccine Candidate from an
TITLE OF INVENTION: Extraintestinal Strain of E. coli
FILE REFERENCE: 11520.0214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 167; Conservative 127; Mismatches 304; Indels 247;
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CURRENT FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 8
LENGTH: 725
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ORGANISM: Escherichia coli
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                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/265,714
APPLICATION UNMBER: US 08/265,714
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BRODERICK, THOMAS F
REGISTRATION NUMBER: 31,332
                                                     TELEFAX: (206) 224 0779
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCE:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTENSEN, O'CONNOR, JOHN
ADDRESSEE: 2800, 1420 FIFTH AVENUE
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: 07-JUN-95
               SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acid
                                                                                                      REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BESSER, THOMAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                             ASWLGARYRGKTPRFTQNYSSLSAVQKKVYDEKGEYLKAWTVVDAGLSWKWTDALTLNAA
                                                                                                                               GXXXXXTLPLWSEDVTLSLNYTWTRSEQRDGDNK--GAPLSYTPEHMVNAKLNWQITEEV
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VMNLLNKDYSDVSLYSAGKSTLYAGDYFQTGSSTTGYVIP--ERNYWMSLNYQF
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RESULT 7
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
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                                                                                                                                                                                                                          E: Christensen, O'Connor, Johnson and Kindness
2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage COMPUTER: Diskette-3.5 inch, 1.44Mb storage COMPUTER: DISKette-3.5 inch, 1.44Mb storage COMPUTER: IBM PC compatible/Pentium OPERATING SYSTEM: MS-Windows-6.0
SOFTWARE: Word for Windows-6.0
CURRENT APPLICATION DATA: WS-Windows-6.0
APPLICATION NUMBER: US/08/765,081
FILING DATE: March 26, 1997
PRIOR APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INPORMATION:
NAME: Shelton, Dennis K.
NAME: Shelton, Dennis K.
NAME: Shelton, Dennis K.
NAME: Shelton, Dennis K.
TELEPHONE: 1-206-682-8100; 1-206-224-0718 (direct)
TELEPHONE: 1-206-682-8100; 1-206-224-0718
INPORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                           STREET: 2800 Pacifi
CITY: Seattle
STATE: Washington
COUNTRY: USA
GENERAL INFORMATION:
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325 L---TAINQFLTVGGEWRHDKLSDAVNLTGGTSSKTSASQYAL--FVEDEWRIFEPLALT 379
                                                           426 ANARKGVRGYSHTVATENLDEFGIYGKS-----TFHPADGLSLIGGGRLGHYKIESGE 478
                                                                                                          380 T----GVR--------MDDHETYGEHWSPRAYLVYNATDTVTVKGG-------413
                                                                                                                                                                                                                                                                                                532 GNQFEVG--YKGS------YMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA 576
                                                                                                                                                                                                                                                                                                                                         577 ALGKRV-------MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL 624
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                                                                                                                                                                                                                                       414 WATAFKAP----------SLLQLSPDWTSNSCRGACKIVGSPDLKPET 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09098082
Patent No. 6040421
GENERAL INFORMATION:
APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
TITLE OF INVENTION: Bscherichia Coli 0157:H7 Epithelial Adhesin NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Center, 1420 Fifth Avenue
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REGISTRATION NUMBER: 35,356
REPERBUCS/DOCKET NUMBER: CHOR-1-12402
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
TELERAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 7:
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APPLICATION NUMBER: US 08/765,081
FILING DATE: March 26, 1997
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: WORD FOR Windows-6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,082
PRILING DATE:
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LENGTH: 663 amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:

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US-09-098-082-7
                                                                                                                                       Sequence 9, Application PC/TUS9506994 GENERAL INFORMATION:
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              APPLICANT:
APPLICANT:
TITLE OF IN
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APPLICANT:
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                                                                                                                                                                                                                                 RAGVLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WATAFKAP----
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                                                                                                                                                                                                                                                             QINADNI 690
                                                                                                                                                                                                                                                                                                                                                       ANGRRIPVFSYYNVNKARNQGVETELKIPFNDEWKLSINYTY--NDGRDVSNGENKPLSD
                                                                                                                                                                                                                                                                                                                                                                                                                  SESWELGLYYMGEEGWLEGVESSVTVFRND-VKDRISISRTSDVN-AAPGYONFVGFETG
                                                                                                                                                                                                                                                                                                                                                                                                                                               GNOFEVG--YKGS------YMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKL-----LKPRQ 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANARKGVRGYSHTVATENLDEFGIYGKS-----TFHPADGLSLIGGGRLGHYKIESGE 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGADWN-KFKM---NSHDVFADLKHYFGNGGYGKVGMRYSDRDADS-----NYA-- 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAE
                                                                                                                                                                                                                                                                                            L-PFHLALEDWSFY--
                                                                                                                                                                                                                                                                                                                       LMPKHSA-NLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKL 683
                                                                                                                                                                                                                                                                                                                                                                                  ALGKRV------MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL
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 ဝှု
              T: BESSER, THOMAS E
T: VARY JR, JAMES C
INVENTION: ESCHERICHIA COLI 0157:H7
SEQUENCES:
                                                 Children's Hospital & Medical Center University of Washington Washington State University Research TARR, PHILLIP I BILGE, SIMA S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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20.8%; Pred. No. 2.6e-15;
ative 106; Mismatches 240
                                                                                                                                                                                                                                                                                        - VSGHYTGQKRADSATAKTPGGYTIWNTGAAWQVIKDVKL
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              EPITHELIAL ADHESIN
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                                                                                         Foundation
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 224 07: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: ESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BRODERICK, THOMAS F
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: CHOR-18591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMEDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: E. coli CirA protein amino acid sequence,
DESCRIPTION: wherein "Xaa" residues represent gaps
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LENGTH: 703 amino acids
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APPLICATION NUMBER: US 0
FILING DATE: 24-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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DESCRIPTION: SEC
DESCRIPTION: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: WA 98101
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                                                                                                                                                                                                                                                                                                   DALGGVVNIITKKIGQKW------SGTVTVDTTIQ-----
                                                                                                                                                                                                                                                                                                                                                                                             RGYE--YSEYNIDGLPAQMQSINGTLPN------LFAFDRVEVMRGPSGLFDSS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA--
                                    VGLGTEIKQKALAFDASYSRPFRLGNTANEFV-IGADY-----
                                                                                                                                                                                                                                                            PRPAEKNNRHETFYAAADWDINP--DTVLGA---GYLYQQRHLAPYNGLPADANNKLPSL
                                                                                                                                                                                                                                                                                                                                                                          RGLDSSYTLILVDG--KRVNSRNAVFRHNDFDLNWIXXXPVDSIERIEVVRGPMSSLYGS
PGNSSPITSESNTVDGKYTLPL---TAINOFLTVGGEWRHDKLSDAVNLTGGTSSKTSAS
                                                                                                                                                  --EGFSSRDGNVEFAWTPNQNHDFTA-----GY---GFDRQDRDSDSLDKNXXXXX
                                                                                                                                                                                   PQHVFVGADWN-KFKM---NSHDVFADLKHYFGNGGYGKVGMRYSDRDADS-----
                                                                                                                                                                                                                       ----EHRDRGDT-YNGQFFTSGPLIDGVLGMKAYGSLAKREKDDPQNSTTTD-TGETPRI
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T: SUITE 2800, 142
SEATTLE
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                                                                                                             -----NYAFAGSKLGMKTPAGRPGCNTADDK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         introduced to facilitate best alignment with SEQ ID NO:8.
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O FIFTH AVENUE
                                                                         GRWDYGTSELKYYGEKVENKNXXXXXXXXXXXXXXX 332
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                                    -NRFRSTNEQGRTT 404
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390 QYAL--FVEDEWRIFEPLALTT----GVR-------MDDHETYGEHWSPRAYLVYNA 433
                                                                                      458 ADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQ 517
                                                                                                                                  -----SLLQLSPDW 459
                                                                                                                                                                               518 INLDADGKL------YRPRQGNQFEVG--YKGS------YMDDRLNARVSFY 555
                                                                                                                                                                                                                                                                       --MEGVETEISGAVTPKWQIHAG 603
                                                                                                                                                                                                                                                                                                                 519 RTSDVN-AAPGYQNFVGFETGANGRRIPVFSYYNVNKARNQGVETELKIPFNDEWKLSIN 577
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                                                                                                                                                                                                                                                                                                                                                                                            405 LYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKS-----TFHP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tarr, P.I., Bilge, S.S., Besser, T.E., Vary Jr., J.C.
TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Christensen, O'Connor, Johnson and Kindness 2800 Pacific First Center, 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sednence
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REGISTRATION NUMBER: 26,997
REGISTRATION NUMBER: CHOR-1-10286
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0718 (direct)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
CMPUTER: IBM PC compatible/Pentium
OPERATING SYSTEM: MS Window 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
DESCRIPTION: Vibrio cholerae IrgA amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/765,081
FILING DATE: March 26, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                  434 TDTVTVKGG-------WATAFKAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGYATFDAMAAYRFTPKLKLQINADNI 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                628 PGGYTIWNTGAAWQVTKDVKLRAGVLNL 655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08765081 Patent No. 5798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio Cholerae
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
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amino acid
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STATE: Washington
COUNTRY: USA
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Length 652;

DB 1,

5.6%; Score 212;

Query Match

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70 TDALKSVPGVTVTGGGDTTDISIRGMGSNYTLILVDGKRQTSRQTRPNSDGPGIEQGWLP 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 ANFFUTGPLSDALSLQVYGQTTQRDEDEIEHGYGDKSLRSLTSKLNYQLNPDHQLQLEAG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 YLYQQRH-----LAPYNGLPADANNKLPSLPQHVFVGADWNKFKMN----SHDVFADLKH 304
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ilarity 19.6%; Pred. No. 7.4e-11;
Conservative 99; Mismatches 299; Indels 204; Gaps
                                                                                                                                           ---LREIPQSVSIITNQQVKDRNVDTF 93
                                                                                                                                                                                                                                    10 SLSVTLGLMFSASAFAQDATKTDETMVVTAAGYAQVIQNAPASISVISREDLESRYYRDV 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 GSLNSDGSVRGRVMAQTVGASPRPAEKNNRH-----ETFYAAADWDINPD--TVLGAG
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TITLE OF INVENTION: Escherichia Coli 0157:H7 Epithelial Adhesin
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seatule
STATE: Mashington
                                                                                                                                                                                                                                                                                                                                       94 DQLARKTPGLRVLSNDDGRS-SVYARGYEYSEYNIDGLPAQMQSI----
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44Mb storage
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Local Similarity
                                                                                                                                           57 SFAVTVGTKIPAS.
                                            Matches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-098-082-6
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Best Local Similarity
Matches 147; Conserv
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FILING DATE: March 26, 1997
APPLICATION NUMBER: PCT/US95/06994
FILING DATE: June 7, 1995
APPLICATION NUMBER: US 08/265,714
FILING DATE: June 24, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
DESCRIPTION: Vibrio cholerae IrgA amino acid sequence
HYPOTHETICAL: NO
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    521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: CHOR-1-12402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 TDALKSVPGVTVTGGGDTTDISIRGMGSNYTLILVDGKRQTSRQTRPNSDGPGIEQGWLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSLNSDGSVRGRVMAQTVGASPRPAEKNNRH-----ETFYAAADWDINPD--TVLGAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLOAIERIEVIRGPMSTLYGSDAIGGVINIITRKDQQQWSGNVQLSTVVQENRASGDEQS
DADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN-----PNN---KK 572
                                        G-----VSTGFRAPQLREVTPDWGQVSG-GGNIYGNPDLQPETSINKELSLMYSTGSGL
                                                                                                                          DEWALAEQFRLTFGGR----
                                                                                                                                                                                                      MLSFGVEGKHESLE------AGFIE 369
                                                                                                                                                                                                                                                                                          ---QGDWQGVGQSDTYLQYEENTNKSREMSIDNTVF---KSTLVAPIGEH-----
                                                                                                                                                                                                                                                                                                                                 YFGNGGYGKVG-----MRYSDRDADS-----NYAFAGSKLGMKTPAGRPGCNTADDKAC 353
                                                                                                                                                                                                                                                                                                                                                                          VSAQDRENNVGKSAQSSGCRGTCSN-----TD-NQYRRNHVAVSH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANFFVTGPLSDALSLQVYGQTTQRDEDEIEHGYGDKSLRSLTSKLNYQLNPDHQLQLEAG
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                                                                               GRLGHYKIESG-EGKTLHKASKT--KFTGYAGAVY---DLNDNNSLYLSLSQLYTPQTNL 520
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OR SEO ID NO: 6:
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                                                                                                                        -----LDHDKNYG-SHFSPRVYGVWNLDPLWTVKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08537361E Patent No. 6121037
GENERAL INFORMATION:
                                                                                                                                                                                      Matches 172;
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
ATHORNEY/AGENT INFORMATION:
RAME: NO. 6121037nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,7
TELECOMMUNICATION INFORMATION:
TELECHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/537,361E FILING DATE: 02-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573 TRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468
118 RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR- 176
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                                       61
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                                                                                                                                                                                    Local Similarity 19.4%; Pr
mes 172; Conservative 103;
                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 14 AATVLAALSSSVFAAQTADLET-----VHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                       IKQEMIRDNKDLVRYSTDVGLSDRSRHQKGFAIRGVEGDRVGVSIDGVNLPDSEENSLYA 120
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                                                                      KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG-----RSSVYA 117
                                                                                                                AALLGSIFGNPVFAADEAATETTPVKAEVKAVRVKGQRNAPAAVER-----VNLNR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYRVNIDEAETYGAEATLSLPITESVELSSSYTYTHSEQKSGNFAGRP--LLQLPKHLFN
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                                                                                                                                                                                                                                                                                                                                            791 amino acids
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IVENTION: No. 6121037el Bacterial Hemoglobin Receptor
IVENTION: Genes and Uses
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So, Magdalene
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                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                          '4.9%; Score 186.5; DB 3; 19.4%; Pred. No. 2.4e-08;
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                                                                                                                                                                                        Mismatches 329;
                                                                                                                                                                                        Indels 283;
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413 LNEFRSIPQVDLIANAR--KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLG 470
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----HKOY 195
                                                                                                           RDLLLPERQFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSQRRGHETESAGKRGY 227
                                                                                                                                                      KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYL 255
                                                                                                                                                                                               228 PVEGAGSGA-NIRGSARG-----IPDPSQ--HKYHSFLGKIAYQINDNHRIGASLN 275
                                                                                                                                                                                                                                            256 YQQRH-----LAPYNGLPADANNK-----LPSLPQHVFVGA--DWNKFKMN 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               592 GAVTPKWQIHAGYSYLHSQ-------IKTASNSRDDGIFLLMPKHSANL 633
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Patent No. 6277382

GENERAL INFORMATION:
APPLICANT: Stojiljkovic, Igor
APPLICANT: Stojiljkovic, Igor
APPLICANT: Hwa, Vivian
APPLICANT: Hwa, Vivian
APPLICANT: Nassif, Xavier
TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
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STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: Illinois
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                                                               ----PTKAF----QGHA-----AAGFGT--
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STATE: Illino:
COUNTRY: USA
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US-08-817-707-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYL 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 R---YGNFNSSRLSIDPELVR-----NIDIVKGADSFNTGSGALGGGVNYQTLQG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 YOORH-----LAPYNGLPADANNK-----LPSLPQHVFVGA--DWNKFKWN 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LNEFRSIPQVDLIANAR--KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 ORDFENLNRDDYYFSGRVVRTTNSIOHPVKTTN---YGFSLSDOIOWNDVFSSRAGIRYD 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 HTKMTPQELNADCHACDKTPPAANTYKGWSGFVGLAAQLSQTWRVGYDVTSGFRVPNASE 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYLSL---SQLYTPQTNLDADGKL----LKPR-----QGNQFEVGYKGSYMDDRLNAR 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283; Gaps
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         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,707
FILING DATE: 19-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6277382man, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-J
TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0001
TELEPHONE: 312-913-0001
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TELEPHONE: 312-913-0001
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4.9%; Score 186.5; DB 4;
Best Local Similarity 19.4%; Pred. No. 2.4e-08;
Matches 172; Conservative 103; Mismatches 329;
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Floppy disk
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 791 amino acida
TYPE: amino acid
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Query Match  4.9%; Score 185; DB 1; Length 792;  Best Local Similarity 19.6%; Pred. No. 3.3e-08;  Matches 173; Conservative 101; Mismatches 335; Indels 274; Gaps 39;  Qy 14 AATVLAALSSSVPAAQTADLETVIKGQRSYNAIVTEKNGDYSSFAVTVGT 64		MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/326,670A FILING DATE: 18 OCT 1994 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: No. 5698438nan, Kevin E REGISTRATION NUMBER: 35,303 REFERENCE/DOCKET NUMBER: 36,784	O. 5698438  INFORMATION: INFORMATION: CANT: Stojiljko CANT: So, Magda CANT: Heaffron, CANT: Heaffron, CANT: Nassif, y OF INVENTION: OF INVENTION: OF SEQUENCES: SPONDENCE ADDREE SPONDENCE SPONDENCE ADDREE SPONDENCE SPONDENCE ADDREE SPONDENCE ADDREE SPONDENCE ADDREE SPONDENCE ADD	Db 576 VSGTPGCTEEDAYYYRCSDPYKEKLDWQMKNIDKARIRGIELTGRLNVDKVA 627  Qy 592 GAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANL 633
APPLICANT: Hefron, Fred APPLICANT: Nessif, Xavier TITLE OF INVENTION: No. 6123942el Bacterial Hemoglobin Receptor TITLE OF INVENTION: Genes and Uses NUMBER OF SEQUENCES: 5 CORRESSONDENCE ADDRESS: ADDRESSE: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive, 32nd Floor CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60806 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	J: J:	596 PKWQIHAGYSYLHSQNPYSEKLEWQMQNIDKARIRGIELTGRLNVDKVASFVP 596 PKWQIHAGYSYLHSQ	Qy 355 VGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALN 414	Db 121 RYGNFNSSRLSIDPELVRNIDIVKGADSFNTGSGALGGGVNYQTLQG 167  Qy 177PTKAFQGHAAAGFGT

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NAME: No. 6277382nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,78
TELECOMMINICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                          ; Sequence 2, Application US/08817707; Patent No. 6277382
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IBM PC compatible
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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Illinois
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US-08-817-707-2
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4.8%; Score 183; DB 3; Length 792;
Best Local Similarity 19.6%; Pred. No. 5.1e-08;
Matches 173; Conservative 101; Mismatches 335; Indels 274;
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: NO. 6123942nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 792 amino acids
TYPE: amino acid
                                                                          APPLICATION NUMBER: US/08/990,470A
FILING DATE: 15-DEC-1997
CLASSIFICATION: 536
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---IKTASNSRDDGIFLLMPKHSANLWTTY 637
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                            65 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG-----RSSVYA 117
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APPLICANT: So, Magdalene
APPLICANT: Waw, Vivian
APPLICANT: Heffron, Fred
APPLICANT: Nassif, Xavier
TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
CORRESPONDENCE ADDRESS:
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300 South Wacker Drive, 32nd Floor
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4.8%; Score 183; DB 4; L
Best Local Similarity 19.6%; Pred. No. 5.1e-08;
Matches 173; Conservative 101; Mismatches 335;
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CURRENT APPLICATION DATA:
FILING DATE: 19-20-1
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RESULT 17
US-08-628-434-4
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APPLICANT: Sparling, P. Frederick
APPLICANT: Beucher, Margaret
TITLE OF INVENTION: Isolated FrpB Nucleic Acid Molecule
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inclone Systems Incorporated
STREET: 180 Varick Street
  STATE: New York
COUNTRY: USA
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,434
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STATE: New York
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  US/08/628,434
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                                              Version
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Best Local Similarity
Matches 171; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PILING DATE: 07-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gallagher Thomas C.
REGISTRATION NUMBER: 37,066
REFERENCE/DOCKET NUMBER: SPA-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-APR-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                        DRFKVKTHDGKTV---SSSSLNPSFGVIWQPREHWSFSASHNYASRSPRLYDALQTHGKR
                                                                                                                                                                                                                                                                                                                 KIEDKKDATEEDKKKNRENEKIAKAYRLTNPTKT--DTGAYIEA-IHEIDGFTLTGGLRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVN--LVRKRPTKAFQGHA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
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                                                                                   ALGKRVMEGVETEISGAVTPKWQIHAGYSYLH-----SQIKTASNSRDDGIFLLMPKH--
                                                                                                                                  GIISIADG--TKAERARNTEIGF--NYNDGTFAANGSYFRQTIKDALA--NPQNR-----
                                                                                                                                                                          ---LDADGKLLKPROGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA
                                                                                                                                                                                                                                                                  GHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSL----YLSLS-QLYTP-QTN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVREEFAVGGENSRITIKRQAPAYRETTQSNTNLAYTGKDLGFVEKLDANAYVLEKKRYS
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----SAN-----LWT---TYQV-TPELTIGGG---VNAMSGITSSAGMH----
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(212) 645-2054
                                                                                                                                                                                                                                                                                                                                                           -----KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRL
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                                            ----HDSVAVREAVNAGYIKNHGYELGASYRTGGLTAKVGVSRSKPRFYD
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COUNTRY:
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----PHSQR-W 694
                                              ----AGGYATFDAMAAYRFTPK--LKLQINADNIFNRHYYARVGGANTFNIPGSERTW 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Children's Hospital & Medical Center
APPLICANT: University of Washington
APPLICANT: Washington State University Research Foundation
APPLICANT: TARK, PHILIP I
APPLICANT: BESSER, PHOMAS E
APPLICANT: BESSER, THOMAS E
APPLICANT: BESSER, THOMAS E
APPLICANT: VARY JR, JAMES C
TITLE OF INVENTION: ESCHERICHIA COLI 0157:H7 EPITHELIAL ADHESIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8%; Score 180.5; DB 5; Length 718;
18.8%; Pred. No. 7.4e-08;
iive 92; Mismatches 285; Indels 255;
                                                                                                                                                                                                                                                                                                                                                                                                           E: CHRISTENSEN, O'CONNOR, JOHNSON AND KINDNESSPLLC SUITE 2800, 1420 FIFTH AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae IrgA amino acid sequence,
wherein Xaa" residues represent gaps
introduced to facilitate best alignment with
SEQ ID NO:6.
                                                               |: :: : | | : | | 647 KLENVVRQGFGVNDVFANWKPLGKDTLNVNLSVNNVFDKFYY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
AURINI APPLICATION DATA:
AUBLICATION NUMBER: PCT/US95/06994
FILING DATE: 07-UUN-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/265,714
FILING DATE: 24-UTN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BRODERICK, THOMAS F
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: CHOR-18591
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                     GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 amino acids
TYPE: amino acids
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Best Local Similarity 18.8°
Matches 146; Conservative
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MOLECULE TYPE: DESCRIPTION:
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ZIP: WA 98101
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ORIGINAL SOURCE:
ORGANISM: VIB
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DESCRIPTION:
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243 DINPD--TVLGAGYLYQQRH------LAPYNGLPADANNKLPSLPQHVFVG- 285
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92 TFDQLARKTPGLRVLSNDDGRS----SVYARGYEYSEYNIDGLPAQMQSI------ 137
                                                         70 DVTDALKSVPGVTVXXXTGGGDTTDISİRGMGSNYTLILVDGKRQTSRQTRPNSDGPGIE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 NTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTV 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----LDHDKNYG-SHFSPRVYGVWNLDPLWTVKGG-----VSTG-----FRAPQLREVT 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             593 AVTPKWOIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAM 652
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                                                                                                                                                                                                                                                                                                                                          190 G----DEQSANFFVTGPL-SDXALSLQVYGQTTQRDEDEIEHGYGDKSLRSLT--SKLNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 ----NYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 XXMSIDNTVF---KSTLVAPIGEH------DMLSFGVEGKHESLE-----D
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APPLICANT: So, Magdalene
APPLICANT: Hwa, Vivian
APPLICANT: Hefron, Fred
APPLICANT: Massif, Xavier
APPLICANT: Nassif, Xavier
TITLE OF INVENTION: No. 6121037el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                     138 NGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHA-
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300 South Wacker Drive, 32nd Floor
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CITY: Chicago
STATE: Illinois
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Matches
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INFORMATION FOR SEQ ID NO: 2:
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NAME: NO. 6121037nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 94,784-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,361E
FILING DATE: 02-OCT-1995
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 792 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 792 amino acid
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                                                                                                                                                                                                                                                        403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 R---YGNFNSSRLSIDPELVR-----NIDIVKGADSFNTGSGALGGGVNYQTLQG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
580 DVSCTQMNYYYGMCS-----NPYSEKLEWQMQNIDKARIRGIELTGRLNVDKVASFVP 632
                                         551 RVS-----FYRMKDKNAAAPLNPNNKKTRYAA--LGKRVMEGVE------TEISGAVT 595
                                                                                                                                                                                                                                                                                                                                                                            355 VGLGTEIKOKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEOGRTTLYARGGLALN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 SHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 PVEGAGSGA-NIRGSARG------IPDPSQ--HKYHSFLGKIAYQINDNHRIGASLN 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 AATVLAALSSSVFAAQTADLETVHI------KGQRSYNAIVTEKNGDYSSFAVTVGT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 19.4
mes 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADMDINPDTVLGAGYL 255
                                                                                                                                                                                                                                                  DFENLNRDDYYFSGRVVRTTSSIQHPVKTIN---YGFSLSDQIQWNDVFSSRAGIRYDHT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOOGHNYTVEESYNLLASYWREADDVNRRRNTNLFYEWTPESDRLSMVKADVDYOKTKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDLLLPERQFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSQRRGHETESAGKRGY 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFAVRGVEGNRVGVSIDGVNLPDSEENSLYA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG-----RSSVYA 117
                                                                                                                                                                                                                                                                                              EFRSIPQVDLIANAR---KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHY 472
                                                                                                                                                                                                        KIESGE-GKTLHKASKTK------FTGYAGAVYDLN------DNNSLYL--SLSQLY 514
                                                                                                                                                                                                                                                                                                                                       ----TRFKRITLRLD---SHPLQLGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PTKAF-----QGHA-----AAGFGT-----HKQY 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AALVGSIFGNPVFAADEAATETTPVKAEVKAVRGKGQRNAPAAVER------VNLNR 60
                                                                                FTYNHGSGNWLPNPNLKAERTTTHTLSLQGRSEKGTLDANLYQSNYRNFLSEEQKLTTSG
                                                                                                                          ----TPQTNLDAD----LNA 550
                                                                                                                                                               KMTPQELNAECHACDKTPPAANTYKGWSGFVGLAAQLNQAWRVGYDITSGYRVPNASEVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.8%; Score 180; DB 3; Length 792; 19.4%; Pred. No. 9.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 328; Indels 284; Gaps
                                                                                                                                                                                                                                                                                                                                       --GRHRLSFKTFASRR 402
                                                                                  579
                                                                                                                                                                   519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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	Ş	KTASNSRD
	문	633 EGWKLFGSLGYAKSKLSGDNSLLFTQPLKVIAGIDYESPSEKWGVFSRLTYLGAK 687
	Q	638QVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFN 692
	문	688 KVKDAQYTVYENKGWGTPLQKKVKDYPWLNKSAY-VFDMYGFYKPVKNLTLRAGVYNVFN 746
	ργ	693 RHY
	<b>Д</b>	747 RKYTTWDSLRGLYSYSTINSVDRDGKGLDRYRAPGRNYAVSLEWKF 792
	RESULT US-08-9 ; Seque	20 537-361 ence 6,
	 ନୁଷ୍	INFORMATION:
	٠. ٠.	Hef
		Nassif, Xavier
		OF INVENTION: NO. 012103/61 Baccellar Hemograms OF SECTEMBES. 14
		CE ADDRESS:
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		IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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	•. •.	Y/AGENT INFORMATION:
	٠. ٠.	,303
		ATION INFORM
	 <del>.</del>	EOF SEO ID NO. 6
		H: 792 am
	; ; ;	TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein 8-537-361E-6
•	Quer Best Matc	4.7%; Score 179; DB 3; Length 792; Best Local Similarity 19.8%; Pred. No. 1.2e-07; Matches 175; Conservative 96; Mismatches 338; Indels 274; Gaps 40
	Ş	14 AATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64
	뮍	10 AALVGSIFGNPVFAADEAATETTPVKAEVKAVRVKGQRNAPAAVERVNLNR 60
	Ş	65 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
	В	61 IKQEMIRDNKDLVRYSTDVGLSDSGRHQKGFAVRGVEGNRVGVSIDGVNLPDSEENSLYA 120
	Ş	YEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMCGIVNLVRKR-   :
	문	121 RYGNFNSSRLSIDPELVRNIDIVKGADSFNTGSGALGGGVNYQTLQG 167

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DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVN--LVRKRPTKAFQGHA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 INPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWN---KFKMNSHDVFA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ADSNYAFAGSKLGM--KTPAG----RPGCNTAD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -NRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIY 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380 KDKEKATNEEKKKN-----RENEKIAKAYRLTNPTK------TDTGAY 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476 GRSPRLYDALQTHGKRGIIS-----IADG--TKAERARNTEIGF--NYNDGTFAAN 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 YSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVT------PELTIGGG---VNAMS 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --------KVDNAYSDŠQILYHQGRF--IVDPALVKVSVQKGAGSA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --KDYEAGKGFRNDNGGKTVPYSALDKRSYLAKIGTTFGDGDHRIVLSHMKDQHRGIRTV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKACAVGLG-----TEIKOKALAFD------ASYSRPFRLGNTANEFVIGADY-- 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 AAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASP--RPAEKNNRHETFYAAADWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VR----LNSGF-----AGNNGASYGASVF-GKEGNFDGLFSYNRNDE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 DLKHYFG-----NGG----YGKVGMRYSDRD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTG------YA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G---AVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 VSFYRMKDKNAAAPLNPNNKKTRYAA----LGKRVMEGVETEIS---GAVTPKWQIHAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 GSYFRQTIKDALA--NPQNRHDSVAVREAVNAGYIKNHGYELGASYRTGGLTAK----VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
4.6%; Score 173; DB 4; Length 713;
Best Local Similarity 19.0%; Pred. No. 3.7e-07;
Matches 163; Conservative 107; Mismatches 277; Indels 310;
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,964
FILING DATE: 07-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gallagher, Thomas C.
REGISTRATION NUMBER: 37,066
REPRENCE/DOCKET NUMBER: SPA-3-P
TELECOMMUNICATION:
TELEPHONE: (212) 645-1405
                                                                                                                                                                                                               INFORMATION:

TELEFAX: (212) 645-1405

TELEFAX: (212) 645-2054

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 713 ami-
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 713 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-628-434-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                                                                                                                                      A----NNYKGSFPIEDSSTLTRNYNQKDLDEIY--------NKSMD---- 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TRFKRITLRLD---SHPLQLGGGRHRLSFKTFASRRDFENLNRD----YYYFSGRV 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TPQTNLDAD-----GKLLK-PRQGNQFEVGYKGSYMDDR---LNA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTYNHGSGNWLPNPNLKAERSTTHTLSLQGRSEKGTLDANLYQSNYRNFLSEEQKLTTSG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVS-----FYRMKDKNAAAPLNPNNKKTRYAA--LGKRVMEGVE-----TEISGAVT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVSCTQMNYYGMCS-----NPYSEKLEWQMQNIDKARIRGIELTGRLNVDKVASFVP 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 VGLGTEIKQKALAFDASYSRPFRLGNTAN--EFVIGADYNRFRSTNEQGRTTLYARGGLA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRTTSSI-------QHPVKTTN---YGFSLSDQIQMNDVFSSRAGIRYDHT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                596 PKWQIHAGYSYLHSQ------IKTASNSRDDGIFLLMPKHSANLWTTY 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÖYTVYENKĞWĞTPLQKKVKDYPWLNKSAY-VFDMYGFYKPVKNLTLKAGVYNVFNKKYTT 751
                                                                                                               KAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYL
                                                                                                                                                   276 GOGGHNYTVEESYNLLASÝWREADDVNRRRNTNLFYEWTPESDRLSMVKADVDYQKTKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY--
                                                                                                                                                                                                                              YQQRH------LAPYNGLPADANNK-----LPSLPQHVFVGA--DWNKFKMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHY
                                                   RDLLLPERQFGVMMKNGYSTRNREWTNTLGFGVSNDRVDAALLYSQRRGHETESAGKRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIESGE-GKTLHKASKTK------FTGYAGAVYDLN------DNNSLYL--SLSQLY
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APPLICANT: Sparling, P. Frederick
APPLICANT: Sparling, P. Frederick
APPLICANT: Bencher, Margaret
TITLE OF INVENTION: Isolated FrpB Nucleic Acid Molecule
UNDMERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----YARVG-----GANTFNIPGSERTWTANLRYSF 722
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,434
FILING DATE: 05-APR-1996
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CITY: New York
COUNTRY: USA
----PTKAF-----QGHA------AAGFGT--
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US-08-613-009A-18
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                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (416) 595-
TELEFAX: (416) 595-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
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APPLICANT: Klein,
TITLE OF INVENTION:
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       159
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                                                                                                                                         58
                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stewart, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 08-MAR-1996
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LFDSSGEMGGIVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA 217
                                 IRGMDKNRVSLTVDGL-AQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGSNS 159
                                                                                                                                                                                                       QFMSVFRIN----MTAATVLAALSSSVFA--AQTADLETVHIKGQRSYNAIVTEKNGDYSS
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                                                                                                                                   FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
                                                                                                                                                                     QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG---- 57
                                                                   -RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR---VEVMRGPSG 158
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                                                                                                                                                                                                                                                                                                                                                                            915 amino acids
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JENTION: Transferrin Receptor Genes
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Harkness, Robin E
Loosmore, Sheena M.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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21.4%; Pred. No. 5.5e-07;
tive 99; Mismatches 292;
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                                                                                                                                                                                                                                                                       Length 915;
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RESULT 23
US-08-778-570B-24
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Pattent No. 6437096
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                       COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,570
                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                  TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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FILING DATE:
                                                                                                                                                                 STATE:
                                                                                                                                                                               CITY: Toronto
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                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLYLSLSQLYTPQTNLDADGKLLKP--RQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - FADLKHYFGNGGYGKVGMRYSDRDA- ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRIGGAEALLIRTGRHA-----GEIRAHEAAGRG-VQSFNRLAPVDDGSKYAYFIVEE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEQGSGALAGSV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -EMYGWRSGDKIKAVKIDPEKSFNK 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAPLNPN--NKKTRYAALGKRVMEGVETEISGAVTPKW-QIHAGYSY----LHS---QIK 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKF-----TGYAGAVYDLNDNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----YDRQGIGLDNHFQ---QTHCSAD---GSDKYCRPSADKPFSYYKSDRVIYGES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTTLYARGGLAL-NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG----IYGKSTFH 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLFTSGENNAPVGAEYGTGVFYDETHTKSRYGLEYVYTNADKD--TWADYARLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFENKRHYIG-GILERTQQTFDTRDMTVPAFLTKAVFDANQKQAGSLRGNGKYAGNHKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECKNG----GHEKCKANPPKDVVGEDKRQTVSTRDYTGPNRFLADPLSYESRSWLFRPGF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---NGLPADANNKLPSLPQHVFVGADW------NKFKMN--SHDV-----
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                                                                                                                                                                 Ontario
                                                                                                                                                                                                  6th Floor,
                                                                                                                                                                                                                                                                                   Klein, Michel H
                                                                                                                                                                                                                                                                                                 Yang, Yan-Ping
                                                                                                                                                                                                                                                                                                                   Du, Run-Pan
                                                                                                                                                                                                                                                                                                                                    Loosmore,
                                                                                                                                                                                                                                                                                                                                                  Harkness, Robin E
                                                                                                                                                                                                                                                                                                                                                                  Schryvers,
                                                                                                                                                                                                                                                                                                                                                                                      Myers, Lisa E
                                                                                                                                                                                    Sim & McBurney
Sim & McBurney
A Floor, 330 University Avenue
03-JAN-1997
                                                                                                                                                                                                                                                    Transferrin
                                                                                                                                                                                                                                                                                                                                    Sheena M.
               US/08/778,570B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           693
                                                                                                                                                                                                                                                                  Receptor Genes
                                               Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----DSNYAFAGSKLGMKTPAGR----P 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RWADVGAGLRYDYRSTHSDDGSVS
                                                                                                                                                                                                                                                                   of Moraxella
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655 -EMYGWRSGDKIKAVKIDPEKSFNK 678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 915 amino acida
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 21.43
Matches 172, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                            ADDAL.
STREET: 6...
TOTONTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                RESULT 24
US-09-059-584-24
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                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LGKLVKTADTLSKEOVLD----IRDLTRYDPGIAVVEOGRGASSGYS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 IRGMDKNRVSLTVDGL-AQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGSNS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 -RGYEYSEYN--IDGLPAQMQS----INGTLP-----NLFAFDR---VEVMRGPSG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRIGGAEALLIRTCRHA-----GEIRAHEAAGRG-VQSFNRLAPVDDGSKYAYFIVEE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PADLKHYFGNGGYGKVGMRYSDRDA-----DSNYAFAGSKLGMKTPAGR---P 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 ----YDRQGIGLDNHFQ---QTHCSAD---GSDKYCRPSADKPFSYYKSDRVIYGES--- 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----TGYAGAVYDLNDNN 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----HKLLQAAFKKSFDTAKIRHNLSVNLGYDRFGSNLRHQD 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 AAPLNPN--NKKTRYAALGKRVMEGVETEISGAVTPKW-QIHAGYSY----LHS---QIK 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             569 YTDCTPRSINGKSYYAAVRDNVRLG------RWADVGAGLRYDYRSTHSDDGSVS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613 TASN---SRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 RFENKRHYIG-GILERTQQTFDTRDMTVPAFLTKAVFDANQKQAGSLRGNGKYAGNHKYG 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG 401
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             3 OFMSVFRIN----MTAATVLAALSSSVFA--AQTADLETVHIKGORSYNAIVTEKNGDYSS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 LFDSSGEMGGIVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA
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                                                                                                                                                                                                                                                                                                                            Query Match 4.6%; Score 173; DB 4; Length 915; Best Local Similarity 21.4%; Pred. No. 5.5e-07; Matches 172; Conservative 99; Mismatches 292; Indels 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --NKFKMN--SHDV----
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            ATTORNEY AGENT INFO 359
ATTORNEY AGENT INFO 351
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24971
REPERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                      linear
    CLASSIFICATION:
                                                                                                                                                                                                                                            ; STRANDEDNESS:
; TOPOLOGY: lir
US-08-778-570B-24
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160 VEQGSGALAGSV------AFQTKTADDVIGEGROWGIQSKTAYSGKNRGLTQSLALA 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 LFDSSGEMGGIVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 QFMSVFRIN----MTAATVLAALSSSVFA--AQTABLETVHIKGQRSYNAIVTEKNGDYSS 57
                                                                  APPLICANT: Myers, Lisa E
APPLICANT: Schryers, Anthony B
APPLICANT: Barkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Do, Nun-Pan
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%; Score 173; DB 4; Length 915; 21.4%; Pred. No. 5.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC Compatible
OPERATE: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99; Mismatches 292;
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6th Floor, 330 University Avenue
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PRIOR APPLICATION NUMBER: US 08/778,570
APPLING DATE: 03-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/09/059,584
14-APR-1998
Sequence 24, Application US/09059584 Patent No. 6440701 GENERAL INFORMATION:
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1031
TELECOMMUNICATION INFORMATION:
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RESULT 25
US-08-487-890A-96
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STREET:
Ontario
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                    CLASSIFICATION:
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      APPLICATION DATA
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Yang, Yan-Ping
Murdin, Andrew
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                                          07-JUN-1993
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Best Local Similarity 21.4%; Pred. No. 6.9e-07;
Matches 172; Conservative 100; Mismatches 291;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acids
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: 11
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REGISTRATION NUMBER: 24,973
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TASN---SRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF
                                                                                                                                AAPLNPN--NKKTRYAALGKRYMEGVETEISGAVTPKW-QIHAGYSY----LHS---QIK 612
                                                                                                                                                                                                                                                                     SLYLSLSQLYTPQTNLDADGKLLKP--RQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG
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                                                                    YTDCTPRSINGKSYYAAVRDNVRLG-
                                                                                                                                                                                                                                                                                                                                                                                                             PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKF-
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618 TGTHRTLSWNAGIVLKPADWLDLTYR 670 DAWAATRFTPKLK-LOINADNIFNR 693 655 -EMYGWRSGDKIKAVKIDPEKSFNK 678 656 -EMYGWRSGDKIKAVKIDPEKSFNK 678 657 -EMYGWRSGDKIKAVKIDPEKSFNK 678 658 -EMYGWRSGDKIKAVKIDPEKSFNK 678 669-363-124A-2 8 GENERAL INFORMATION: APPLICANT: Spalling, P. Frederick APPLICANT: Cornelissen, Cynthia N. TITLE OF INVENTION: Transferrin-Bindi TITLE OF INVENTION: Nisseria Genorrh NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSEE: IMClone Systems Incorpor STREET: 180 Varick Street CITY: New York COUNTRY: USA ZTATE: New York COUNTRY: USA ZTATE: New York COUNTRY: USA ZTATE: New York COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZTATE: New YORK COUNTRY: USA ZOFTWARE: DEC-1994 CLLASSITCATION DATA: APPLICATION NUMBER: US O7/973,336 FILING DATE: 23-AUG-1993 ATTORREY PREFACE TO TO NUMBER: SPA-1-PDC TELECOMMUNICATION NUMBER: 37,066 REFERENCE COUNTRY: STATION TO TELECOMMUNICATION NUMBER: 37,066 REFERENCE COUNTRY: USA TELEPRAN: (212) 645-204 TELEPRAN: (212) 645-204 TELEPRAN: (212) 645-204 TELEPRAN: SEQ ID NO: SEQ ID NO: SEQUENCE TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-1-PDC TELECOMMUNICATION NUMBER: MUNDEN: SPA-	4 OV 159 LPDSSGEMGGI		Oy 218 OTVGASPRPAE	Db 211 GRIGGAEALLI Ov 265NGLPADAN	263	Qy 299 - FADLKHYFGN	319	Qy 344 GCNTADDKACA	Db 378 GLFTSGENNAP	Qy 402 RTTLYARGGLA	Db 430YDRQGIG	Qy 457 PADGLSLIGGG	Db 477	LĀTŌSTSTĀTS 505 KŌ	:       Db 515 YYYQSANRAYS	Qy 563 AAPLNPNNK	Db 569 YIDCTPRSING	Qy 613 TASNSRDD	618	Qy 670 DAMAAYRFTPK	Db 655 -EMYGWRSGDK	RESULT 27 US-08-478-435-96 : Sequence 96. Applia	; Patent No. 5922323 ; GENERAL INFORMATIO	; APPLICANT: LOOS				STREET:		-
D D O O O O O O O O O O O O O O O O O O	::	DAMAAYRFTPKLK-LQINADNIFNR	-   :   :     :   :   :   :   :   :   :	ULT 26 08-363-1248-2	equence 2, Application US/08363124A atent No. 5912336	GENERAL INFORMATION: APPLICANT: Sparling, P. Frederick	N. Binding	seria Gonorrhea	CORRESPONDENCE ADDRESS: ADDRESSEE: Imclone Systems Incorporated	·	STATE: New York COUNTRY: USA	ZIP: 10014 COMPUTER READABLE FORM:	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/363,124A	FILING DATE: 23-DEC-1994 CLASSIFICATION: 536	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/124,254	FILING DATE: 20-SEP-1993 PRIOR APPLICATION DATA:	APPLICATION NUMBER: US 07/973,336 FILING DATE: 05-NOV-1992	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/572,187	FILING DATE: 23-AUG-1990 ATTORNEY/AGENT INFORMATION:	REFERENCE/DOCKET NUMBER: SPA-1-PDC TELECOMMUICATION: INFORMATION: TELEPHONE: (212) 645-1405	TELEFAX: (212) 645-2054 INFORMATION FOR SEQ ID NO: 2:	T	ino acid linear PE: protein	tch 4.6%; Score 172; DB 2; Length 915; al Similarity 21.4%; Pred. No. 6.9e-07; 172: Conservative 100; Mismatches 291; Indels 242;	QFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYS		FAVTVGTKIPASLREIPQSVSIIINQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA	EGREVATADILDSREGVEDIRDEIRIDFGLAVEGGRGASSGIS

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IRTGRHA-----GEIRAHEAAGRG-VQSFNRLAPVDDGSKYAYFIVEE 262
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IVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA 217
                                                                                                                                                                                        NNKLPSLPQHVFVGADW------ 298
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                                                                                                                                                                                                                                                                                                                    -GILERTQQTFDTRDMTVPAFLTKAVFDANQKQAGSLRGNGKYAGNHKYG 377
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Schryvers, Anthony
Schryvers, Anthony
Minong, Pele
Sray-Owen, Scott
Ang, Yan-Ping
Hurdin, Andrew
Liein, Michel
RWION: Transferrin Receptor Genes
UNENCES: 147
Exampless: 18 Andrew
Sim & McBurney
Sim & McBurney
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Floppy disk
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LTENTIN Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:

US/08/478,435

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Best Local Similarity
Matches 172; Conserv
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 96
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
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FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRGMDKNRVSLTVDGL-AQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGSNS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFMSVFRIN---MTAATVLAALSSSVFA--AQTADLETVHIKGQRSYNAIVTEKNGDYSS 57
                                                                                                                                                                                                  GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG 401
                                                                                                                                                                                                                                          RFENKRHYIG-GILERTQQTFDTRDMTVPAFLTKAVFDANQKQAGSLRGNGKYAGNHKYG
                                                                                                                                                                                                                                                                                  -FADLKHYFGNGGYGKVGMRYSDRDA------DSNYAFAGSKLGMKTPAGR---P 343
                                                                                                                                                                                                                                                                                                                                                              ---NGLPADANNKLPSLPQHVFVGADW------NKFKMN--SHDV-----
                                                                                                                                                                                                                                                                                                                                                                                                         GRIGGAEALLIRTGRHA-----GEIRAHEAAGRG-VQSFNRLAPVDDGSKYAYFIVEE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                               QTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPY------
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                                   PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKF-----TGYAGAVYDLNDNN
                                                                                                                    RTTLYARGGLAL-NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG----IYGKSTFH 456
                                                                                                                                                            GLFTSGENNAPVGAEYGTGVFYDETHTKSRYGLEYVYTNADKD--TWADYARLS-----
                                                                                                                                                                                                                                                                                                                        ECKNG----GHEKCKANPKKDVVGEDKRQTVSTRDYTGPNRFLADPLSYESRSWLFRPGF 318
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                                                                              GSDKYCRPSADKPFSYYKSDRVIYGES---
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                                                                                                                                                                                            US-08-337-483-96
                                                                                                  Query Match
Best Local Similarity 21.4%; ...
172; Conservative 100;
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                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/337
APPLIANG DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
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                                                                                                                                                                                                                                               TYPE:
                                                                                                                                                                                                                                                                                                                   TELEFAX:
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TOPOLOGY: linear
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                                                                                     QFMSVFRIN---MTAATVLAALSSSVFA--AQTADLETVHIKGQRSYNAIVTEKNGDYSS
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                                                    QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG----
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Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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Schryvers, Anthony
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                                                                                                                       4.6%; Score 172; DB 2;
21.4%; Pred. No. 6.9e-07;
tive 100; Mismatches 291;
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                                                                                                                                                      Length 915;
                                                                                                                       Indels 242;
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                                           -RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR---VEVMRGPSG 158
                                                                                  101 IRGMDKNRVSLTVDGL-AQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGSNS 159
                                                                                                                                LFDSSGEMGCIVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA 217
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                                                                                                                                                                                                                        QTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPY------ 264
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APPLICANT: Harkness, Robin
APPLICANT: Gray-Vers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-Ping
APPLICANT: Mirdin, Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Mirdin, Andrew
APPLICANT: Mirdin, Andrew
ANDRER OF INVENTION: Transferrin Receptor Genes
CORRESPONDENCE ADRESS:
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Suite 701, 330 University Avenue
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655 -EMYGWRSGDKIKAVKIDPEKSFNK 678
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Patent No. 5922841
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CITY: Toronto
STATE: Ontario
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ZIP: M5G 1R7
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US-08-478-373-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---NGLPADANNKLPSLPQHVFVGADW------NKFKMN--SHDV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 915;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: .07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
4.6%; Score 172; DB 2; L
Best Local Similarity 21.4%; Pred. No. 6.9e-07;
Matches 172; Conservative 100; Mismatches 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1038-463 MIS:vg
                                                                                                                                                                                                         FILING DATE: 07-UN-1955
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION NUMBER: US 08/337,483
FILING DATE: 29-DEC-1993
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/148,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    915 amino acids
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STRANDEDNESS: si
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RESULT 30
US-08-474-671-96
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                    TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
TITLE OF IN
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Transferrin Receptor Genes
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                                                                      TELEPHONE: (416) 595-1155
                                                                                                                                                             FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION:
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                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 29-DEC-1993
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                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EMYGWRSGDKIKAVKIDPEKSFNK 678
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Suite 701, 330 University Avenue
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Yang, Yan-Ping
Murdin, Andrew
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Harkness, Robin
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                                                                                                                                                                                                US 08/148,968
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Sequence 96, Application US/08483577A
Patent No. 6015688
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena
APPLICANT: Harkness, Robin
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-474-671-96
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RESULT 31
US-08-483-577A-96
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Best Local :
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                                                                                                          670 DAMAAYRFTPKLK-LQINADNIFNR
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                                                                             655 -EMYGWRSGDKIKAVKIDPEKSFNK
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                                                                                                                                                                                                                                                               AAPLNPN--NKKTRYAALGKRVMEGVETEISGAVTPKW-QIHAGYSY----LHS---QIK 612
                                                                                                                                                                                                                                                                                                                                         SLYLSLSQLYTPQTNLDADGKLLKP--RQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTTLYARGGLAL-NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG----IYGKSTFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFENKRHYIG-GILERTQQTFDTRDMTVPAFLTKAVFDANQKQAGSLRGNGKYAGNHKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECKNG----GHEKCKANPKKDVVGEDKRQTVSTRDYTGPNRFLADPLSYESRSWLFRPGF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---NGLPADANNKLPSLPQHVFVGADW---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG----
                                                                                                                                                       TGTHRTLSWNAGIVL --- KPADWLDLTYR
                                                                                                                                                                                        TASN---SRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF
                                                                                                                                                                                                                              YTDCTPRSINGKSYYAAVRDNVRLG------RWADVGAGLRYDYRSTHSDDGSVS
                                                                                                                                                                                                                                                                                                      YYYQSANRAYSLKTPPQNNGKKTSPNGREKNPYWVSI-----GRGNVVTRQICLFGNNT
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Pred. No. 6.9e-07;
0; Mismatches 291;
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-FADLKHYFGNGGYGKVGMRYSDRDA------DSNYAFAGSKLGMKTPAGR---P 343
                                                                                                                              319 RFENKRHYIG-GILERTQQTFDTRDMTVPAFLTKAVFDANQKQAGSLRGNGKYAGNHKYG 377
                                                                                                                                                                                                              378 GLFTSGENNAPVGAEYGTGVFYDETHTKSRYGLEYVYTNADKD--TWADYARLS----- 429
                                                                                                                                                                                                                                                                                    402 RITLYARGGLAL-NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG----IYGKSTFH 456
                                                                                                                                                                                                                                                                                                                                    ----YDROGIGLDNHFQ----QTHCSAD---GSDKYCRPSADKPFSYYKSDRVIYGES--- 476
                                                                                                                                                                                                                                                                                                                                                                                       457 PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKF------TGYAGAVYDLNDNN 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 SLYLSLSQLYTPQTNLDADGKLLKP--RQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              515 YYYQSANRAYSLKTPPQNNGKKTSPNGREKNPYWVSI-----GRGNVVTRQICLFGNNT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 AAPLNPN--NKKTRYAALGKRVMEGVETEISGAVTPKW-QIHAGYSY----LHS---QIK 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 569 YIDCTPRSINGKSYYAAVRDNVRLG------RWADVGAGLRYDYRSTHSDDGSVS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TASN---SRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF 669
                                                                                                                                                                                 344 GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TSTGFRLPSFA-- 654
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APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Yang, Pele
APPLICANT: Wardin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: 07-UUN-1995
PRIOR PRIOR DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US 08/337,483
08-NOV-1994
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; Sequence 96, Application US/08897438
; Patent No. 6262016
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ADDRESSEE: Sim & MCF
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CLASSIFICATION: 435
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ZIP: M5G 1R7
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GENERAL INFORMATION:
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ilarity 21.4%; Pred. No. 6.9e-07;
Conservative 100; Mismatches 291; Indels 242;
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                     APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Gray-Owen, Scott
APPLICANT: Wandin, Andrew
APPLICANT: Windin, Andrew
APPLICANT: Klein, Michel
ITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
BILING DATE: 08-NOV-1994
PRIOR APPLICATION NUMBER: US 08/175,116
PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 29-DEC-1993
PRILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
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CLASSIFFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1038-511
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION UNDHER: 24,973
REFRENCE/DOCKET UNDHER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INPORMATION FOR SEQ ID NO: 96: SEQUENCE CHARACTERISTICS:
LENGTH: 915 amino acida
TYPE: amino acida
TYPE: amino acida
TYPE: amino acida
TYPE: amino acida
TYPE: amino acida
TYPE: amino acida
     Schryvers, Anthony
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Best Local Similarity
Matches 172; Conserva
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ZIP: M5G 1R7
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PRIOR APPLICATION DATA:

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INFORMATION FOR SEQ ID NO: 1
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LENGTH: 915 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-NOV-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                     344
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  569 YTDCTPRSINGKSYYAAVRDNVRLG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 GRIGGAEALLIRTGRHA------GEIRAHEAAGRG-VQSFNRLAPVDDGSKYAYFIVEE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 IRGMDKNRVSLTVDGL-AQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGSNS 159
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 QFMSVFRIN---MTAATVLAALSSSVFA--AQTADLETVHIKGQRSYNAIVTEKNGDYSS 57
                                                                                                                                                                                                                                                                                                                                                 GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEQGSGALAGSV-----AFQTKTADDVIGEGRQWGIQSKTAYSGKNRGLTQSIALA
                                    AAPLNPN--NKKTRYAALGKRVMEGVETEISGAVTPKW-QIHAGYSY----LHS---QIK 612
                                                                                                                 SLYLSLSQLYTPQTNLDADGKLLKP--RQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNA 562
                                                                                                                                                                                          PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKF-----TGYAGAVYDLNDNN 504
                                                                                                                                                                                                                                                                      RTTLYARGGLAL-NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG----IYGKSTFH 456
                                                                                                                                                                                                                                                                                                             GLFTSGENNAPVGAEYGTGVFYDETHTKSRYGLEYVYTNADKD--TWADYARLS-----
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                                                                                                                                                                                                                                ----YDRQGIGLDNHFQ---QTHCSAD---GSDKYCRPSADKPFSYYKSDRVIYGES---
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21.4%; Pred. No. 6.9e-07;
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-- RWADVGAGLRYDYRSTHSDDGSVS
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                                                                                                                                                                                                            Query Match
Best Local 9
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                                                                                                                                                                                             Matches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-AUG-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES NUMBER OF SEQUENCES: 147
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101 IRGMDKNRVSLTVDGL-AQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGSNS
                             118 -RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR----VEVMRGPSG 158
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                                                               58
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                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                        TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                           QFMSVFRIN---MTAATVLAALSSSVFA--AQTADLETVHIKGQRSYNAIVTEKNGDYSS
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                                                                                             FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
                                                                                                                              QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG----
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M5G 1R7
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Gray-Owen, Scott
Yang, Yan-Ping
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Klein, Michel H
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                                                               LGKLVKTADTLSKEQVLD-----IRDLTRYDPGIAVVEQGRGASSGYS 100
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21.4%; Pred. No. 6.9e-07;
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GRIGGAEALLIRTGRHA-----GEIRAHEAAGRG-VQSFNRLAPVDDGSKYAYFIVEE 262
                                                                                                                                                                     ---NGLPADANNKLPSLPQHVFVGADW------NKFKMN--SHDV----- 298
                                                                                                                                                                                                             ECKNG----GHEKCKANPKKDVVGEDKRQTVSTRDYTGPNRFLADPLSYESRSWLFRPGF 318
                                                                                                                                                                                                                                                         -FADLKHYPGNGGYGKVGMRYSDRDA-----DSNYAFAGSKLGMKTPAGR---P 343
                                                                                                                                                                                                                                                                                   RTTLYARGGLAL-NEFRSIPQVDLIANARKGVRGYSHTVATENLDEFG----IYGKSTFH 456
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159 LFDSSGEMGGIVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA 217
                                                                                                                                                                                                                                                                                                                                        GCNTADDKACAVG--LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG 401
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                                                                                                                                                                                                                                                                                                                                                                                378 GLFTSGENNAPVGAEYGTGVFYDETHTKSRYGLEYVYTNADKD--TWADYARLS-----
                                                                                 QTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPY
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APPLICANT: Harkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Murdin, Andrew
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Mindin, Andrew
APPLICANT: Riein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
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ZIP: MSG 1R7
COMPUTER REABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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6th Floor, 330 Unviersity Avenue
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Patent No. 6361779
GENERAL INFORMATION:
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ADDRESSEE: Sim & MCE
STREET: 6th Floor, 3
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4.6%; Score 172; DB 4; Length 915;
Best Local Similarity 21.4%; Pred. No. 6.9e-07;
Matches 172; Conservative 100; Mismatches 291; Indels 242; 457 PADGLSLIGGGRLGHYKIESGEGKTLHKASKTKF----FILING DATE: 07-UN-1995
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
FRIOR APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-608
TELECOMMUNICATION INFORMATION: CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,518
FILING DATE: 17-MAY-1996 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577 (416) 595-1155 TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: 915 amino acids single TYPE: amino acid STRANDEDNESS: siz linear CLASSIFICATION: TELEPHONE: US-08-649-518-96 LENGTH: 28 565 599 430 원 8 셤 à ò 셤 ò 8 ò 8 8 ò 셤 ò d

Query Match 4.5%; Score 171; DB 2; Length 909; Best Local Similarity 18.2%; Pred. No. 8.4e-07; Matches 180; Conservative 128; Mismatches 327; Indels 356; Gaps 49;	; INFORMATION FOR SEQ ID NO. 4: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 909 amino acids ; TYPE: amino acids ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-363-124A-4	; REGISTRATION NUMBER: 37,066 ; REFERENCE/DOCKET NUMBER: SPA-1-PDC ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (212) 645-1405 ; TELEPAX: (212) 645-2054	APPLICATION NUMBER: US 07/572,187 ; FILING DATE: 23-AUG-1990 ; ATTORNEY/AGENT INFORMATION: ; NAME: Gallagher, Thomas C.	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 07/973,336 ; FILING DATE: 05-NOV-1992 ; PRIOR APPLICATION DATA:	525	; SOFTWARE: PatentIn Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/363,124A ; FILING DATE: 23-DEC-1994	罗马马恩	CITY: New York STATE: New York COUNTRY: USA ZIP: 10014	BEQUENCES: 8 RICE ADDRESS: IMClone Systems Incorporated 180 Varick Street	APPLICANT: Sparling, P. Frederick APPLICANT: Cornelissen, Cynthia N. TITLE OF INVENTION: Transferrin-Binding Proteins From TITLE OF INVENTION: Neisseria Gonorrhea and Neisseria Meningitidis	4 H W W	Db 655 -EMYGWRSGDKIKAVKIDPEKSFNK 678	670 DAMAAYRFTPKLK-LOINADNIFNR 693	QY 613 TASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATF 669	569 YTDCTPRSINGKSYYAAVRDNVRLGRWADVGAGLRYDYRSTHSDDGSVS	Db 515 YYYQSANRAYSLKTPPQNNGKKTSPNGREKNPYWVSIGRGNVVTRQICLFGNNT 568 OV 561 AAPLNPNNKKTBYAALGKRVMRGVETETSGAVTPKW-OTHAGYGYTHSOIK 612	Db 477
RESULT 36 US-08-817-707-8 ; Sequence 8, Application US/08817707 ; Patent No. 6277382	823 696 879	Qy 615 SNSRDDGIFLLMPKHSANLWTTYQVTPELTI 645	Qy 564 APLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTA 614	Qy 519 NLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSF-YRMKDKNAA 563	Qy 480KTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT 518	Qy 433 RGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEG 479 : :   :   :   :	Qy 377 RIGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGV 432	Qy 317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376	OY 257 QORHLAPYNGLPADANNKLPSLPQHVFVGADMNKFKMNSHDVFADLKHYFGNGGYGKVGM 316	Qy 234 ETFYAAADWDINP	Qy 204 SLNSDGSVRGRVMAQTVGASPRPAEKNNRH 233	QY 172LVRKRPTKAFQGHAAAGFGTH	Db 158 NSSEYGNGALAGSVAFQTKTAADIIGEGKQWGIQSKTAYSGKDHALTQSLALAGRSGGAE 217		116	Qy 56 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTPDQLARKTPGLRVLSNDDGRSSV 115	QY 3 QFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDY 55

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908 amino acids
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FRY: Canada
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STRANDEDNESS: sin
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US-08-613-009A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 NSSRLSIDPELVR------NIEIAKGADSFNTGSGALGGGVNY-----QTLQGHD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRH----- 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|: | :: : | |:: :: | | EGAGSGAIIRGSSRGIPDPSK--HKYHNFLGKIAYQINDKHRIGPSFNGQQGHNYTIEES 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHY-----FGNGG-- 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---YGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 NIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGH- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- AAAGFGTHKQYKAEADVSGSLNS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 YNLTASSWREADDVNR----RRNANLFYEWTPDSNWLSSLKADFDYQTTKVAAVNNKGSF 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 FDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIAN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 LAALSSSVF----AAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLRE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 IAALVGSIFGNPVLAADEAATETTPVKAEIKEVRVKDQLNAPATVERVNLGRIQQEMIRD 68
                                                                 APPLICANT: Hwa, Vivian
APPLICANT: Heffron, Fred
APPLICANT: Heffron, Xavier
TITLE OF INVENTION: No. 6277382el Bacterial Hemoglobin Receptor
TITLE OF INVENTION: Genes and Uses
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
4.5%; Score 169.5; DB 4; Length 790;
Best Local Similarity 18.5%; Pred. No. 9.2e-07;
Matches 153; Conservative 102; Mismatches 336; Indels 235;
                                                                                                                                                                                                            ADDRESSEB: McDonnell Boehnen Hulbert & Berghoff STREET: 300 South Wacker Drive, 32nd Floor CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-AUG-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 6277382nan, Kevin E
REGISTRATION NUMBER: 35,303
REPERSINCE/DOCKET NUMBER: 94,784-J
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/817,707
19-AUG-1997
                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 790 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-707-8
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
GENERAL INFORMATION:
                   APPLICANT:
APPLICANT:
APPLICANT:
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378 MD---SQPLQLG------GRHRLSLKTFASRREFENLNRDDYYFS 413
                                                                                                                                485 ASKTK-----FTGYAGAVYDLN-----DNNSLYL--SLSQLY-----TPQ 517
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                                                                                                                                                                                                                                                                                                                                                                 --- IKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGV 649
                                                                                        428 AR--KGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE-GKTLHK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                             557 MKDKNAAAPLNPNNKKTRYAA--LGKRVMEGVE-----TEISGAVTPKWQIHAGYSYL 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643 KSKLSGDNSLLSTQPPKVIAGIDYESPSEKWGVFSRLTYLGAKKAKDAQYTVYENKGRGT 702
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APPLICANT: Harkness, Robin E
APPLICANT: Hosenore, Sheena M.
APPLICANT: Losenore, Sheena M.
APPLICANT: Yang, Yan-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Transferrin Receptor Genes of Moraxella
UNDBER OF SEQUENCE: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650 NAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            703 PLOKKVKDYPWLNKSAY-VFDMYGFYKLAKNLTLRAGVYNVFNRKY 747
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,009A
FILING DATE: 08-MAR-1996
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-542
TELEPRATION INFORMATION:
TELEPRAX: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 16, Application US/08613009A; Patent No. 6090576
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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Query Match Best Local Similarity

4.5%; Score 169.5; DB 3 18.0%; Pred. No. 1.2e-06;

DB 3;

Length

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                                                                                                                                                                                                        NARIAGINILGKIDWHGV-------WGGLPDGLYSTLAYNRIKVKDA-DIRADRTF
                                                                                                                                                                                                                                        KTRYAA----LGKRVMEGVETEISGAVTPKW-----QIHAGYSYLHSQIKTASNSRDDGIF 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLDNRLOQTHCSHDGSDKNCRPDGNKPYSFYKSDRMI-----YEESRNLFQAVFKKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----IRLIVKSSDTLSKEQVLN----IRDLTRYDPGIAVVEQGRGASSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQNAVQAYDLITPPKPPFPNGSKDNPYRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGLFDSSGEMGGIVN-------
                                                                                                                                                                    LKPEKSFNREAGIVFKGDFGNLEASYFNNAYRDLIAFGYETRTQNGQTSASGDPGYRNAQ
                                                                                                                                                                                                                                                                                                                                              HSEDKSVSTGTHRNLSWNAGVVLKPFTWMDLTYRASTGFRLPSFAEMYGWRAGESLKTLD
                                                                                                                                                                                                                                                                                                                                                                              HKASKTKFTG-----YAGAV-----YDLNDNNSLYL---SLSQLYTPQTNLDADGKL
                                                                                                                                                                                                                                                                                                                                                                                                                IGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRLGRW-ADVGAGIRYDYRST
                                                                                                                                                                                                                                                                                                                                                                                                                                               HTVATENLDEFGIYGKSTFHPADGLSLIGGG------RIGHYKIESGEG-----KTL 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTFDTRDMTVPAYFTSE-DYVPGSLKGLGKYSGDNKAERLFVQGEGSTLQGIGYGTGVFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFMSVFRINMTAATVLAALSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY 55
                                                                 -KKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRYVTWENVROTAGGAVNOHKN 886
                                                                                                 ITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY------YAR 698
                                                                                                                                  VTSYLFDAVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDELLGSQALLNGNANA---
                                                                                                                                                                                                                                                                                                           LKPRQGNQFEVG--YKG-----SYMDDRLNARVSF-YRMKDKN-----AAAPLNPNNK 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLKEDASVKDERKTVSTODYTGSNRLLANPLEYGSQSWLFRPGWHLDNRHYVGAVLERTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSIRGMDKNRVSLTVDGV-SQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQQHLFRLNILCLSLMTAL -- PVYAENVQAEQAQEKQLDTIQVKAKKQKTRRDNEVTG-- 57
                                VGGANTFNI PGSERTWTANLRY 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 125;
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ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,570B
FILING DATE: 03-JAN-1997
CLASSIFICATION: 536
CTASSIFICATION: 536
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 24973
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APPLICANT: Harkness, Robin B
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Xang, Yan-Ping
APPLICANT: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
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STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
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Patent No. 6440701
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APPLICANT: Myers, Lisa E
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56 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115 116 YA-RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR---VEVMRGP 156 SGLFDSSGEMGGIVN NSSEYGNGALAGSVAFOTKTAADIIGEGKOWGIOSKTAYSGKDHALTQSLALAGRSGGAE 217 278 KLKEDASVKDERKTVSTQDYTGSNŔLLANPLEYGSOSWLFRPGWHLDNRHYVGAVLERTQ 337 338 QTPDTRDMTVPAYFTSE-DYVPGSLKGLGKYSGDNKAERLFVQGEGSTLQGIGYGTGVFY 396 257 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316 DERHIKNRYGV----YARLSYDRQGI 432 317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376 DLDNRLQQTHCSHDGSDKNCRPDGNKPYSFYKSDRMI-----YEESRNLFQAVFKKAF 485 377 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYS 436 HTVATENLDEFGIYGKSTFHPADGLSLIGGG------RLGHYKIESGEG-----KTL 482 544 IGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRLGRW-ADVGAGIRYDYRST 602 603 HSEDKSVSTGTHENLSWNAGVVLKPFTWMDLTYRASTGFRLPSFAEMYGWRAGESLKTLD 662 218 ALLIYTKRRGREIHAHKDAGKGVQSFNRLVLDEDKKEGGSQYRYFIVEEECHNGYAACKN 277 Gaps 3 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY 55 DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQNAVQAYDLITPPKPPPPNGSKDNPYRVS HKASKTKFTG-----YAGAV----YDLNDNNSLYL---SLSQLYTPQTNLDADGKL SLNSDGSV---RGRVMAQTVGASPR----PAE-----KNNRH------Query Match
4.5%; Score 169.5; DB 4;
Best Local Similarity 18.0%; Pred. No. 1.2e-06;
Matches 177; Conservative 125; Mismatches 341; UMBER: US 08/778,570 03-JAN-1997 ---LVRKRPTKAFQGHAAAGFGTH-----ETF-----YAADWDINP------FILING DATE: 03-ZAN-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS: 14-APR-1998 LENGTH: 908 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear PRIOR APPLICATION DATA: APPLICATION NUMBER: TOPOLOGY: US-09-059-584-22 157 158 172 234 397 483 유 음 ð ò ð ò ò

ATION: hael I 24,973 -24,973 MBER: 1038-466 MIS ORWATION: 95-1155 -1163 NO: 94: ICS: acids le	COUNTRY: Canada ZIP: M52 1R7 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Vers SOFTWARE: Patentin Release #1.0, Vers APPLICATION NUMBER: US/08/487,890A FILING DATE: 07-JUN-1993 CLASSIFICATION: 435 PRIOR APPLICATION UNMBER: US 08/175,116 FILING DATE: 29-DEC-1993 PRIOR APPLICATION NUMBER: US 08/175,116 FILING DATE: 29-DEC-1993 PRIOR APPLICATION NUMBER: US 08/148,968 FILING DATE: 08-NOV-1993	US-08-487-890A-94  ; Sequence 94, Application US/08487890A ; Patent No. 5708149 ; GENERAL INFORMATION:    APPLICANT: LOOSMOORE, Robin APPLICANT: Harkness, Robin APPLICANT: Chong, Pele ; APPLICANT: Gray-Owen, Scott APPLICANT: Wang, Yan-Ping APPLICANT: Wang, Yan-Ping APPLICANT: Murdin, Andrew APPLICANT: Klein, Michel ; TITLE OF INVENTION: Transferrin Receptor NUMBER OF SEQUENCES: 147 CORRESPONDENCE ADDRESS:    ADDRESSEE: Sim & McBurney STREET: 6th Floor, 330 Unviersity Aven CITY: Toronto STATE: Ontario	Qy 527 LKPRQGNQFEVGYKGSYMDDRLNARVSF-YRMKDKNAAAPLNPNNK
MIS: jb	e	ptor Genes Avenue	RLNARVSF-YRMKDKNAAAPLNPNNK 571

	YARVGGANTENIPGSERTWTANLRY 720 	
	647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY 695         ;   ;   ;   ;   ;   ;   ;   ;	Оу 6.
	616 NSRDDGIFLLMPKHSANLWTTYQVTPELTIG 646	Qy 6: Db 7:
	564 APLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTAS 615	Qy 51
	19 NLDADGKLLKPROGNQFEVGYKGSYMDDRLNARVSF-YRMKDKNAA 563	. Qy 5:
	80KTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT 518	Qy 41
	33 RGYSHTVATENLDEFGIYGKSTEHPADGLSLIGGGRLGHYKIESGEG 479	Qγ 4: Db 5:
	77 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGV 432	Qy 3:
	17 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376	Db . 4:
	157 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316 	Qy 25 Db 39
	4. 00	Qy 23 Db 33
	204 SLNSDGSVRGRVMAQTVGASPRPAEKNNRH 233	Qу 2; Db 2;
	172LVRKRPTKAFQGHAAAGFGTH	Qy 17 Db 21
	157 SGLFDSSGEMGGIVN 171 	. Db 15
	116 YA-RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGP 156	Oy 1
3.	56 SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115	אלם קל
	3 QFMSVERINMTAATVLAALS8SVFAAQTADLETVHIKGQRSYNAIVTEKNGDY 55	δ .δ
49;	y Match 4.4%; Score 167.5; DB 1; Length 908; Local Similarity 18.2%; Pred. No. 1.8e-06; hes 180; Conservative 125; Mismatches 330; Indels 355; Gaps	Query Ma Best Loo Matches

us-09-889-267-2.rai

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APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Michal, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       696 ----YARVGGANTFNIPGSERTWTANLRY 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 94, Application US/08337483; Patent No. 5922562; GENERAL INFORMATION:
                                                                    ---LVRKRPTKAFQGHAAAGFGTH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loosmore, Sheena
Harkness, Robin
Schryvers, Anthony
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-337-483-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                          234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 YA-RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR---VEVMRGP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ------LGKLVKSSDTLSKEQVLN-----IRDLTRYDPGIAVVEQGRGASSG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QOQHLFRINILCLSIMTAL -- PVYAENVQAEQAĞEKQLDTIQVKAKKQKTRRDNEVTG -- 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
                                                                                                                                                                                 APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Wirdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1038-462 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPLICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIPEICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION NUMBER: US 08/175,116
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                           Sequence 94, Application US/08478435 Patent No. 5922323
                                                                                                             Loosmore, Sheena
Harkness, Robin
Schryvers, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (416) 595-1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: Bi
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: Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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ETF-----DIVLGAGY---LY 256 QTPDTRDMTVPAYFTSE-DYVPGSLKGLGKYSGDNKAERLFVQGEGSTLQGIGYGTGVFY 396 257 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316 397 DERHTKNRYGV------EXVYHNAD-----KDTWAD----YARLSYDRQGI 432 317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376 433 DLDNRLQQTHCSHDGSDKNCRPDGNKPYSFYKSDRMI-----YEESRNLFQAVFKKAF 485 377 RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR----KGV 432 486 DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQ------NAVQAYDLITPKKPPFPNGS 535 RGYSHTVA----TENLDEFGIYGKSTFHPADGLSLIGGG------RLGHYKIESGEG 479 :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | : 655 GESLKTLDLKPEKSFNREAGIVFKGDFGNLEASYFNNAYRDLIAFGYETRTQNGQTSASG 714 564 APLNPNNKKTRYAA---LGKRVMEGVETEISGAVTPKW----QIHAGYSYLHSQIKTAS 615 715 DPGYRNAQNARIAGINILGKIDWHGV------WGGLPDGLYSTLAYNRIKVKDA- 762 616 NSRDDGIFL-----VTPELTIG 646 763 DIRADRIFVTSYLFDAVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDELLGSQALLN 822 218 ALLIYTKRRGREIHAHKDAGKGVQSFNRLVLDEDKKEGGSQYRYFIVEEECHNGYAACKN 277 KLKEDASVKDERKTVSTODYTGSNRLLANPLEYGSOSWLFRPGWHLDNRHYVGAVLERTQ 337 823 GNANA----KKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRYVTWENVRQTAG 878 ----KTLHKASKTKFTG-----YAGAV-----YDLNDNNSLYL---SLSQLYTPQT 519 NLDADGKLLKPRQGNQFEVG--YKG-----SYMDDRLNARVSF-YRMKDKN----AA 647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY------

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 908 amino acids
; TYPE: amino acid
STRANDEDNESS: single
; TOPOLOGY: linear
US-08-337-483-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Canada
ZIP: M5G 1R7
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
                                                                                                                                                                                                                                            338
486 DTAKIRHNLSINLGYDRFKS--QLSHSDYYLQ-----NAVQAYDLITPKKPPFPNGS 535
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                                                                                                     RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376
                                                                                                                                                          DERHTKNRYGV-----EYVYHNAD-----KDTWAD----YARLSYDRQGI 432
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                                     RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR----KGV 432
                                                                              DLDNRLQQTHCSHDGSDKNCRPDGNKPYSFYKSDRMI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGLFDSSGEMGGIVN-----
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Patentin Releation DATA: ON NUMBER: US/ON TE: 07-JUN-1995 ATION: 435 CATION DATA: ON NUMBER: US ON NUMBER: US ON NUMBER: US ON TE: 08-NOV-1994 ATION: 435 ATION: 435 ATION: 435 ATION: 435 ATION: DATA: ON NUMBER: US ON NUMBER: 24	wen, Scott Yan-Ping , Andrew Michel : Transferrin Rec S: 147 RESS: & McBurney 61, 330 University FORM: oppy disk oppy disk c compatible c compatible c PC-DOS/MS-DOS	SULT 43 Sequence 94, Application US/08478373 Patent No. 5922841 GENERAL INFORMATION: APPLICANT: Loosmore, Sheena APPLICANT: Schryvers, Anthony APPLICANT: Chong, Pele	715 DP 616 NS 616 NS 763 DI 647 GG 823 GN	433 RGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRIGHYKIESGEG 479  536 KDNPYRVSIGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRLGRW-ADVGAG 594  480KTLHKASKTKFTGYAGAVYDLNDNSLYLSLSQLYTPQT 518  595 IRYDYRSTHSEDKSVSTGTHRNLSWNAGVVLKPFTWNDLTYRASTGFRLPSFAEMYGWRA 654  519 NLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSF-YRMKDKNAA 563  655 GESLKTLDLKPEKSFNREAGIVFKGDFGNLEASYFNNAYRDLIAFGYETRFQNGQTSASG 714  564 APLNPNNKKTRYAALGKRVMEGYETEISGAVTPKWQIHAGYSYLHSQIKTAS 615

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3 OFMSVFRINMTAATVLAALSSSVFA-----AQTADLETVHIKGQRSYNAIVTEKNGDY
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STREET: Suite 701, 330 University Avenue
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                                                                                                                                                 ----YARVGGANTFNIPGSERTWTANLRY 720
                                                                                                                                                                           879 GAVNQHKNVGVYNRYAAPGRNYTFSLEMKF 908
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FILING DATE: 07-UN-1995
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
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FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              ; Sequence 94, Application US/08474671; Patent No. 6008326
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CLODDY disk
COMPACING SYSTEM: PC-DOCOMPACING SYSTEM: PC-DOCOMPACE.
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REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 94
                                                                                                                                                                                                                                                                                                                                                          Loosmore, Sheena
Harkness, Robin
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amino acid
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COMPUTER REDABLE FORM:
MEDIUM TYPE: F1~-
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
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APPLICANT: LOOSMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Suite
CITY: Toronto
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REFERENCE/DOCKET NUMBER: 1038-463 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
STRANDEDNESS: single
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US-08-478-373-94
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49; 823 GNANA----KKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRYVTWENVRQTAG 878 647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHY-----Length 908; APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Wurdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Riein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS: Patentin Release #1.0, Version #1.25 Query Match
4.4%; Score 167.5; DB 3;
Best Local Similarity 18.2%; Pred. No. 1.8e-06;
Matches 180; Conservative 125; Mismatches 330;

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RESULT 45
US-08-483-577A-94
; Sequence 94, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NLDADGKLLKPROGNQFEVG--YKG-----SYMDDRLNARVSF-YRMKDKN-----AA
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                                                                                                                          GAVNOHKNYGVYNRYAAPGRNYTFSLEMKF 908
                                                                                                                                                             ----YARVGGANTFNIPGSERTWTANLRY 720
                                                                                                                                                                                              GNANA----KKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRYVTWENVRQTAG 878
                                                                                                                                                                                                                                                                  DIRADRTFVTSYLFDAVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDELLGSQALLN 822
                                                                                                                                                                                                                                                                                                     NSRDDGIFL------WPK------HSANLW-----TTYQ-----VTPELTIG
                                                                                                                                                                                                                                                                                                                                                                           APLNPNNKKTRYAA----LGKRVMEGVETEISGAVTPKW-----QIHAGYSYLHSQIKTAS 615
                                                                                                                                                                                                                                                                                                                                                                                                              GESLKTLDLKPEKSFNREAGIVFKGDFGNLEASYFNNAYRDLIAFGYETRTQNGQTSASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTFDTRDMTVPAYFTSE-DYVPGSLKGLGKYSGDNKAERLFVQGEGSTLQGIGYGTGVFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLNSDGSV---RGRVMAQTVGASPR----PAE------KNNRH------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YA-RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR----VEVMRGP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.4%; Score 167.5; DB 3; Best Local Similarity 18.2%; Pred. No. 1.8e-06; Matches 180; Conservative 125; Mismatches 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE

COMPUTER: PATENT PC-DOS/MS-DOS

SOFTWARE: PATENTIN PC-DOS/MS-DOS

SOFTWARE: PATENTIN PATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,577A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/337,483

FILING DATE: 08-NOV-1994

PRIOR APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION NUMBER: US 08/148,968

APPLICATION NUMBER: US 08/148,968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24 9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Klein, Michel TITLE OF INVENTION: Transferrin Receptor Genes NUMBER OF SEQUENCES: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                     172
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218 ALLIYTKRRGREIHAHKDAGKGVQSFNRLVLDEDKKEGGSQYRYFIVEEECHNGYAACKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
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STREET: Suite 701, 330 Un
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                                   ---LVRKRPTKAFQGHAAAGFGTH-------KQYK-----AEADVSG
                                                                            NSSEYGNGALAGSVAFQTKTAADIIGEGKQWGIQSKTAYSGKDHALTQSLALAGRSGGAE
                                                                                                                   SGLFDSSGEMGGIVN-----
                                                                                                                                                      YSIRGMDKNRVSLTVDGV-SQIQSYTAQAALGGTRTAGSSGAINEIEYENVKAVEISKGS 157
                                                                                                                                                                                             YA-RGYEYSEYN--IDGLPAQMQS-----INGTLP-----NLFAFDR----VEVMRGP 156
                                                                                                                                                                                                                                                                         SSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSV 115
                                                                                                                                                                                                                                                                                                                QQQHLFRLNILCLSLMTAL--PVYAENVQAEQAQEKQLDTIQVKAKKQKTRRDNEVTG-- 57
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M5G 1R7
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Klein, Michel
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Yang, Yan-Ping
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Harkness, Robin
Schryvers, Anthony
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277
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204 SLNSDGSVRGRVMAQTVGASPRPAE	234 ETFYAAADWDINP	257 QQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGM 316	317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376 317 RYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPF 376 433 DLDNRLQQTHCSHDGSDKNCRPDGNKPYSFYKSDRMIYEESRNLFQAVFKKAF 485	377 RLGNTANBFVIGADYNRFRSTNEGGRTTLYARGGLALNEFRSIPQVDLIANARKGV 432 +	433 RGYSHTVATENLDBFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEG 479 : :	480KTLHKASKTKFTGYAGAVVDLNDNNSLYLSLSQLYTPQT 518	519 NLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSF-YRMKDKNAA 563	564 APLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTAS 615	616 NSRDDGIFLLMPKHSANLWTTYQVTPELTIG 646 16	647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLOINADNIFNRHY 695 	696YARVGGANTENIPGSERTWTANLRY 720 
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Search completed: December 18, 2002, 06:47:00 Job time : 28.862 secs

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OM protein - protein search, using sw model
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December 18, 2002, 06:40:34 ; Search time 27.0814 Seconds (without alignments) 2562.980 Million cell updates/sec
                                                                                                                                                                                                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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Title: Perfect score: US-09-889-267-2 3776

MGQFMSVFRINMTAATVLAA......NTFNIPGSERTWTANLRYSF 722

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters:

283224

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database 3 P. H PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Score	% Query Match	Length I	DB	ID	1 1 1 1
μ.	3244	85.9	708	ນ ¦	в81038	TonB-dependent rec
2	832	2	802	2	312	O.
ω	N	1	826	N	S41569	LD
4.	822.5	Ч	813	N	A40601	ferripyoverdine re
U	821.5		815	N	H83345	
6	788	0	725	N	D81976	probable ferric si
7	784	0	725	N	н81030	endent r
80	767.5	0	819	N	S15169	Ωı
9	755		753	N	AE0187	probable iron-side
10	737.5		729	N	C64854	
11	736.5		729	2	H90813	
12	734.5		729	N	D85673	outer membrane rec
13	715.5	18.9	720	N	A36942	Fe(III)-pyochelin
14	708.5		809	N	S32899	ferric-pseudobact
15	512	13.6	863	N	AF2074	ferrichrome-iron
16	486.5		820	N	AE2130	ferrichrome-iron
17	486.5		885	N	AB1944	ferrichrome iron
18	483.5		854	Ν	AE2082	
19	481	12.7	858	Ν	AD2421	ferrichrome iron
20	479	12.7	851	N	D87252	TonB-dependent rec
21	475	12.6	863	N	AI2077	ferrichrome iron
22	470	•	760	Ν	E64817	probable membrane
23	467.5	٠	867	N	AC2140	ferrichrome-iron
24	465	٠	828	N	S74450	ferrichrome-iron
25	460.5	•	851	N	AE2129	ferrichrome-iron
26	460	12.2	760	N	C90739	hypothetical prote
27	460		760	N	E85589	
28	459	12.2	708	N	A83043	OD.
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TVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120

121 EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA

EYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180

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301

361 IKQKALAFDASYSRÞFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIÞ 420

301 DLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTE 360

DLKHYFGNGGYGKVGMRYSDRKADSNYTFAGSKLN-----NTG--QADVAGLGTD

DWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKEKMNSHDVFA 300 FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRRETFYAAA FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAA 240

DWD INPDTVLGAGYLYQQRRLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMHSHDVFA

300

240

180

44	43	42	41	40	39	38	37	36	S	34	33	32	31	30
396.5 391	396.5	402	407.5	411	415.5	416.5	420.5	421.5	424	432.5	441.5	441.5	449.5	450
10.5	10.5	10.6	10.8	10.9	11.0	11.0	11.1	11.2	11.2	11.5	11.7	11.7	11.9	11.9
802 713	710	863	635	714	857	853	853	696	858	732	753	708	872	819
20	N	N	N	N	N	N	N	N	N	N	N	N	N	N
C83588 E91118	S22673	S74447	C81861	C95382	AC2132	S74457	AC2079	AC0547	AE2085	A83481	D83081	AH2626	AC2134	AI3197
probable hydroxama probable ferrichro	ferrioxamine recep	ferrichrome-iron r	hypothetical prote	probable ferrichro	ferrichrome-iron r	ferrichrome-iron r	ferrichrome-iron r	ferrioxamine B rec	ferrichrome-iron r	probable TonB-depe	probable outer mem	ferrichrome iron r	ferrichrome-iron r	TonB-dependent rec

## ALIGNMENTS

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B 8	Quer Best Matc	A; Status: 1 A; Molecule A; Molecule A; Residues A; Cross-re- A; Experime C; Genetics A; Gene: NM	A;Auth A;Titl A;Refe	R;Tett Hickey Ti, H.	RESULT 1 B81038 TonB-dep C;Specie C;Date:
1 MGQFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV 60                1 MGQFMSVFRINMTAATVLAALSSSVFAAQTEGLETVHIKGQRSYNAIATEKNGDYSSFAA 60	Query Match 85.9%; Score 3244; DB 2; Length 708; Best Local Similarity 86.8%; Pred. No. 6.1e-219; Matches 627; Conservative 33; Mismatches 48; Indels 14; Gaps 3;	A;Rectus: preliminary A;Molecule type: DNA A;Residues: 1-708 < TET- A;Residues: 1-708 < TET- A;Cross-references: GB:AE002532; GB:AE002098; NID:g7227078; PIDN:AAF42164.1; PID:g722708 A;Cross-remental source: serogroup B, strain MC58 C;Genetics: C;Genetics: NMB1829	A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307	C;ACCESSION: B81038 R;Tettelin, H.; Salunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.Al Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287 1809-1815 2000	RESULT 1 B81038 TonB-dependent receptor NMB1829 [imported] - Neisseria meningitidis (strain MC58 serogro C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

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C;Species: Pseudomonas ap.
C;Date: 13-3da-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Date: 13-3da-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: 841569; 834357
R;Morris, J; Donnelly, D.F.; O'Neill, E.; McConnell, F.; O'Gara, F.
R;Mol. Gene. 242, 9-16, 1994
A;Title: Nucleotide sequence analysis and potential environmental distribution of a ferr. A;Reference number: 841569; MUID:94104606; PMID:8277948
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A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Cross-references: EMBL:X73412; NID:g313725; PIDN:CAA51812.1; PID:g313726
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo
C;Keywords: membrane procein
F;183-317/Domain: tonB-dependent receptor amino-terminal homology <TNN>
F;540-826/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || : || : :| || :| :| :| 607 LKGEHFGGALNSQIALFQIDQENRATEDVGGPSPCPFSPT---SRYCSRASGKVRSQGVD 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDG--IFLLMPKHSANLWTTYQVTPEL-- 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664 LELSGALSDDWQMAGYTYVDAKYKHDSNKANEGKPFDAAKPRHLFKLATSYTLPGELHK 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TIGGGVNAMSGI-TSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGG 701
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   KVGMRYSDRDADSNYAFAG-----SKLGMKTPAGRPG-CNTADDKACAVGLGTEI 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAA 187
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                                                                      KLA-----ADKLWARINMLGLYNDCYYSTTGCASMTQNPGDYSYTDDHD------
                                                                                                                                               362 KQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGL---ALNEFRS
                                                                                                                                                                                      419 IPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE
                                                                                                                                                                                                                                                                                                                                                      DPSSTLKPRLNTSLWGMK-----LDQEQKGAYLTTRLNLADPLKVILGGRLDWYKADADT
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.larity 29.9%; Pred. No. 8.4e-50;
Conservative 129; Mismatches 303; Indels 101
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349 IKQXAFAVDASYSRPFALGNTANEFVIGADYNRLRSTNEQGRSTL--SKSVALDGFRALP 406
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                                                                                                                    TLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYK
                                                                                                                                                                                                                                                                HAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSSAG
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Best Local Similarity 30.0%; Pred. No. 4.5e-50;
Matches 222; Conservative 137; Mismatches 309; Indels
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A;Title: Characterisation of the pvdB gene which is required A;Reference number: JC5090; MUID:97075909; PMID:8918232 A;Accession: PC4227
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C;Date: 03.May-1994 #text_change
C;Accession: A40601; S54000; PC4227
R;Poole, K.; Neshat, S.; Krebes, K.; Heinrichs, D.E.
J. Bacteriol. 175, 4597-4604, 1993
A;Title: Cloning and nucleotide sequence analysis of the ferripy A;Reference number: A40601; MUID:93328663; PMID:8335619
C;Keywords: membrane protein F;184-317/Domain: tonB-dependent receptor F;538-813/Domain: tonB-dependent receptor
                                                      A;Gene: fpvA
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal
                                                                                                                    A;Cross-references:
C;Genetics:
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A; Residues: 1-49 < MCM>
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A;Residues: 1-715,'Y',717-744,'YN',745-747,'S',749-813 <LAM>
A;Residues: 1-715,'Y',717-744,'YN',745-747,'S',749-813 <LAM>
R;Cross-references: EMBL:U07359; NID:91633044; PIDN.AAB60199.1;
R;McMorran, B.J.; Merriman, M.E.; Rombel, I.T.; Lamont, I.L.
                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: S54000
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amino-terminal homology <TNN>
carboxyl-terminal homology <TNC>
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Query Match
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                                         VGGANTFNI PGSERTWTANLRYSF
                                                                                                                           GGGVNAMSGITSSAG-----MHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYAR
                                                                                                                                                                       EISGELAPGWQVQAGYT--HKIIRDDSGKK---VSTWEPQDQLSIFTSYKFKGALDKLTV
                                                                                                                                                                                                             EISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQ---VTPELTI
                                                                                                                                                                                                                                                                                                FEVGYKGSYMDDRLNARVSFYRMKDKNAAAP-----LNPNNKKTRYAALG-KRVMEGVET
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IGFYTSASY-GDPRNLMFSTRWDF
                                                                                 GGGARWQGKSWQMVNPRRWEKFSQEDYWLVDLMARYQITDKLSASVNVNNVFDKTYYTN
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R;Stover, C.K.; Pham, X.Q.; E. adman, S.; Yuan, Y.; Brody, L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequ.
A;Reference number: A82950; M
A;Accession: H83345
A;Status: preliminary
                                                                                                                                                                                ferripyoverdine receptor PA2398 [imported] - Pseudomonas aeruginosa (strain c;Species: Pseudomonas aeruginosa (c;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: H83345
A; Molecule type: DNA
                                                             sequence of Pseudomonas aeruginosa PA01,
50; MUID:20437337; PMID:10984043
                                                                                                                                           Erwin,
L.L.; C
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K.R.; Kas,
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20.9%; Score 788; DB 2; Length 725; illarity 29.9%; Pred. No. 4.7e-47; Conservative 117; Mismatches 316; Indels 112;

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A,Molecule type: DNA,
A,Residues: 1-725 cPAR,
A,Residues: 1-725 cPAR,
A,Residues: 1-725 cPAR,
A,Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CABB3866.1; PID:g737931
A,Experimental source: serogroup A, strain Z2491
C,Genetics:
A,Gene: NMA0575
C,Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homo
A;Reference DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Accession: D81976 Ab1775; MUID:20222556; PMID:10761919 A;Accession: D81976 A;Status: preliminary A;Molecule rows.
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Matches 232; Conserva
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                                                  GB:AE004091; NID:g9948438; PIDN:AAG05786.1; GSPDB:GN001
                                                                                                        amino-terminal
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                                                                                                                                                                                                                                                                                                                                                          HAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAADWD 243
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                                                                                                                                                                                                                                              ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
                                                                                                                                                                                          FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
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                                  A,Residues: 1-815 <STO>
A,Cross-references: GB:AE004666; GB:AE004091; NID:g9948438; PIDN:AAG0
A,Experimental source: strain PAO1
C,Genetics:
C,Genetics: A3398
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor
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                                                                                                                                  Query Match 21.8%; Score 821.5; DB 2; Length Best Local Similarity 29.0%; Pred. No. 2.5e-49; Matches 217; Conservative 145; Mismatches 312; Indels
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ETFYAAADWDINPDTVLGAGYLYQQRHL---APYNGLPADANNKLPSLPQHVFVGADWNK 290
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                                                                                                      FAVIVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQ-LARKTPGLRVLSNDD--GRSS 114
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                                   5 MSVFRINMTAATVL-----AALSSSVFAAQTADLETVHIKGORSYNAIVTEKNGDYSS 57
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                                                                                                                                                                                                               VYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR
                                                                                                                                                                                                                                                                                                                     KRPTKAFQGHAAAGFGTHKQYKABADVSGSLNSDGSVRGRVMAQ-TVGASPRPAEKNNRH
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RESULT 7 #81030 TonB-dependent receptor NMB1882 [imported] - Neisseria meningitidis (strain MC58 serogrow C;Species: Neisseria meningitidis

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D81976
probable ferric siderophore receptor protein NMA0575 [imported] - Neisseria meningitidia probable ferric siderophore receptor protein NMA0575 [imported] - Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001 C;Accession: D81976
C;Accession: D81976
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MARYRFNPRAELSLNVDNLFNKHYRTQ-----

---PDRHSYGALRTVNAAFTYRF

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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: H81030 R;Tettcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: H81030
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C;Superfamily:
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A; Residues: 1-725 < TET>
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Best Local S
Matches 228
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 MAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIP-----
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                                                                                               NLWTTYQVTPEL---TIGGGV---
                                                                                                                                                               KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA 631
                                                                                                                                                                                                                                                     YTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKN--AAAPLNPNNK
                                                                                                                                                                                                                                                                                           RAADNLSLILGGRYTRYRTGSYDSRTQGMTYVSANRFTPYTGIVFDLTGNLSLYGSYSSL
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                                                         KLFTAYHFAPEAPSGWT1GAGVRWQSETHTDPATLR1PNPAAKARAADNSRQKAYAVADI
                                                                                                                                   NTYYRAANQAKTHGWEIEVGGRITPEWQIQAGYSQSKTRDQDGSRLNPDSV----PERSF
                                                                                                                                                                                                               FVPQSQKDEHGSYLKPVTGNNLEAGIKGEWLEGRLNASAAVYRARKNNLATAAGRDPSG-
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B, strain MC58
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Pred. No. 8.9e-47;
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                                                                                               -NAMSGITSSAGMHAGGYATFDA 671
                     -GSERTWTANLRYSF
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A;Residues: 1-819 <BIT>
A;Cross-references: EMBL:X56605; NID:g45722; PIDN:CAA39942.1;
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A;Accession: S15169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Bitter, W.; Marugg, J.D.; de Weger, L.A.; Mol. Microbiol. 5, 647-655, 1991
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993
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;1-47/Domain: signal sequence #status predicted <SIG>
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EVVPDSG----GLIASRAVDGAETKGVDVELSGEVLPGWNVFTGYS-
                                    ---PNNKKTRYAALGKRVMEGVET----EISGAVTPKWQIHAGYSYLHSQIKTASNSRD
                                                                           ASYTDIFKPONNVDITGKPLDPEVGKNYELGWKGEFLEGRLNANIALYMVKRDNLAESTN
                                                                                                                                                         RFNLTDDLHLILGARASNYRFDYALWRIGNEPAPYKMVERGVVTPYAGIVYDLTNEQSVY
                                                                                                                                                                                            TFHPADGLSLIGGGRLGHYKIE-----SGEGKTLHKASKTKFTGYAGAVYDLNDNNSLY
                                                                                                                                                                                                                                                                                                                                                      GCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPA----DANNKLPSLPQHVFVGADWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FDGVTTYQDNQTRNMPSTLMDVGLYDRIEIVRGATGLMTGAGDPSAVVNVIRKRPTREFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSIRETPQTITVVTRQRMDDQHLGSMNEVLTQTPGI-TMSQDGGERFNIYSRGSAINIYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASLREIPOSVSIITNOOVKDRNVDTFDQLARKTPGLRVLSNDDG-RSSVYARGYEYSEYN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YQIDGNTVTVTASA-----AAKDGQIELSATNVNSAGLGETTEGTGSYTTRVTSTATKWN 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP
                                                                                                                  LSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN
                                                                                                                                                                                                                                                                          TLYARGGLALNEFRSIPQVDL-----IANARKG----VRGYSHTVATENLDEFGIYGKS
                                                                                                                                                                                                                                                                                                                 YLELDGSTEISAGIVT-AKQHQKGVDATLQGPFQLLGQTHELIVGYNYLEYENKH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                    KFKMNSHDVFADLKHYFG-----NGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRP
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NiAlternate names: outer membrane protein fhuE
CiSpecies: Escherichia coli
CiSpecies: Escherichia coli
CiSpecies: Escherichia coli
CiDate: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 01-Mar-2002
CiAccession: G64854; S09362; A26875; PC4409
Riblattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Accession: C64854
A;Molecule type: DNA
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. Bacteriol. 169, 2044-2049, 1987
;Title: Ferric-coprogen receptor FhuE of Escherichia coli: processing and sequence commuserence number: A26875; MUID:87194585; PMID:3032906
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A;Residues: 1-69 <SA2>
R;Kobayashi, Y.; Sasanuma, A.; Nishimura, A.; Kuratomi, K.
Rese. Commun. Biochem. Cell Mol. Biol. 1, 157-170, 1997
A;Title: A novel 14-kilodalton protein in Pl,P4-bis(5'-adenosyl)tetraphosphate (Ap4A)-bin
A;Reference number: JC5685
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(Schuperfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog|
(S.Gywords: iron transport; membrane protein; receptor
(B;1-36/Domain: signal sequence #status predicted <SIG>
(B;1-36/Domain: outer membrane protein fhuE #status predicted <MAT>
(B;97-230/Domain: tonB-dependent receptor amino-terminal homology <TNN>
(B;97-230/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
510 FVPYSGLTYDINRDLSVYTSYTEIFNPENRRDRNNTLLAPVSGQNYEAGLKGVAFDNSLD 569
                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-362,'C',364-729 <SAU>
A;Cross-references: EMBL:X17615; NID:g41448; PIDN:CAA35616.1; PID:g41449
A;Experimental source: strain K-12
                                                                                                                            SYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQV---TPELTIGGGVNAMS----GITS
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A, Residues: 1-47 < KOB>
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: O2-Nov-2001
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Cillingworth, T.; Cronin, A.; Davies, R.W.; Davie, P.; Dougan, G.;
il, M.; Mutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AE0187
A;Residues: 1-753 «KUR»
A;Residues: 1-753 «KUR»
A;Residues: 1-753 «KUR»
A;Residues: 1-753 «KUR»
A;Genetics:
C;Genetics:
A;Gene: YPOL537
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homq
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--EDKNSFVNRYDQSKNPFYGILEIDVTPNTLFTFG-ADTQRTLTRGGMFGGLPLFNSAG 304
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                                     DGIFLLMPKHSANLWTTYQVTPE---LTIGGGVNAMSGITSSAGMH-----AGGYATFDA 671
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                                                                                                                                                                                                                          RINMT----AATVLAALSSSVFAAQTADLETVHIKGQRSYN-
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C;Genetics: A;Gene: ECs1480 C;Superfamily: f

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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yogasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shi DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H99813
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-729 <HAY>
A;Residues: 1-729 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34903.1; PID:g13360944; GS A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                             outer membrane receptor for ferric iron uptake BCs1480 [imported] - Escherichia C;Species: Bscherichia coli C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C;Accession: H90813
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                                                                                                                                                                                                             AMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
                                                                                                                                                                                                                                                                                                                            STGTPIPGSNGETAYKAVDGTVSKGVEFELNGAITDNWQLTFGATRYI-----AEDNEG
                                                                                                                                                                                                                                                                                                                                                                  ---APLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYS-YLHSQIKTASNSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIGSFYN-FNG-
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                                                                                                                                                                                                                                                            NAVNPNLPRTTVKMFTSYRLPVMPELTVGGGVNWQNRVYTDTVTPYGTFRAEQGSYALVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HMKSLYAATRVTLADPLHLILGARYTNWRVDT----LTYSMEKNHTTPYAGLVFDINDNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFFSGIVDADLGDLTTLSAGYEYQRIDVNSPTWGGLPRWNTDGSSNSYDRARSTAPDWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TFYAA-ADWDINPDTVLGAGYLYQQRHL--APYNGLPA-DANNKLPSLPQHVFVGADWNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SREFKGDVSAEYGSWNKERYVADLQSPLTEDGKIRARI----VGGYQNNDSWLDRYNSEK
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                   D.J.;
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                   Apodaca
                                     Mayhew
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A;Title: Genome sequence A;Reference number: A8548 A;Accession: D85673

nence of A85480; I

enterohemorrhagic Escherichia MUID:21074935; PMID:11206551

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0157:H7

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A; Molecule type: DNA
A; Residues: 1-720 <STO>
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                                        PIDN: AAG55848.1; GSPDB:GN00145; UWGP:Z17
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                                                                                                                                                                                        11 QYQAITKPSLLAGCIALALLPSAAXAAPATEETVIVEGSAT---APDDGENDYSVTSTSA 67
                                                                                                                                                Gaps
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                                                                                            receptor
                                                                                                                                               Indels 103;
                                                                                                                     DB 2; Length 729;
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A;Nolecule type: DNA
A;Residues: 1-729 <STO>
A;Residues: 1-729 <STO>
A;Cross-references: GB:AE005174; NID:g12514649; PIDN:AAG55846
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: fhue
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent:
                                                                                                                   Query Match 19.5%; Score 734.5; DB 2; Best Local Similarity 27.1%; Pred. No. 2.6e-43; Matches 209; Conservative 146; Mismatches 313;
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A36942
Fe(III)-pyochelin receptor fptA precursor - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 31-Dec-2000 C;Accession: A36942; G831.77
R;Ankenbauer, R.G.; Quan, H.N.

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M.J.; Br
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83117
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A;Experimental source: strain PAO1
J. Bacteriol. 176, 307-319, 1994
A;Title: FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate A;Reference number: A36942; MUID:94117363; PMID:8288523
A;Accession: A36942
                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: I-720
A;Mcross-references: GB:U03161; NID:g454352; PIDN:AAC43213.1; PID:g454353
A;Cross-references: GB:U03161; NID:g454352; PIDN:AAC43213.1; PID:g454353
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, S;Stover, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, John, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|:|| || || |:: |:|||| :| |
DRYRAEVDVGGPLSASGNVRGRAVA---AYEDRDYFYDVADQGTR--LLYGVTEFDLSPD 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVLGAGYLYQQ-RHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYF 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 IANARKGVR----GYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGK 480
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18.9%; Score 715.5; DB 2;
Best Local Similarity 27.2%; Pred. No. 5.5e-42;
Matches 200; Conservative 137; Mismatches 323;
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A;Gene: pupB
A;Gene: pupB
A;Start codon: GTG
C;Superfamily: ferric-pseudoba
C;Keywords: membrane protein
F;1-45/Domain: signal sequence
F;46-809/Product: ferric-pseud
F;189-319/Domain: tonB-depende
F;543-809/Domain: tonB-depende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Pseudomonas putida (;Date: 31-Dec-1993 #text_change C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change C;Accession: S3289  
R;Koster, M.; van de Vossenberg, J.; Leong, J.; Weisbeek, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Identification and characterization of the pupB A,Reference number: S32899; MUID:93316856; PMID:8392140 A,Accession: S32899
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A;Cross-references: GB:
C;Genetics:
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Best Local Sim
Matches 197;
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;46-809/Product: ferric-pseudobactin receptor #status predicted <MAT>
;46-809/Product: repseudobactin receptor amino-terminal homology <TNN:
;189-319/Domain: tonB-dependent receptor carboxyl-terminal homology <;
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ol. Microbiol. 8, 591-601, 1993
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                                  GKSTFHPADGLSLIGGGRLGHYKIES-----
                                                                         TPSWGGWRYDYAGSPAGAIDNLFNWDGKSAKPAFVESGKSSI.
                                                                                                                                                                                                                                                                                                SQLMYGITEFDLSEDTLLTVGFSYLRSDIDSPLRSGLPTRFSTGERTNLKRSLNAAPDWS
                                                                                                                                                                                                                                                                                                                                   HETFYAAADWDINPDTVLGAGYLYQQRHL-APY-NGLPAD-ANNKLPSLPQHVFVGADWN
                                                                                                                                                                                                                                                                                                                                                                        IRKRPTAEAQASITGEAGNWDRYGTGFDVSGPLTETGNIRGRFVADYKTEKAWIDRYNQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDIDQGLAILLAGTGLEASRGANASYSLQASASTGALELSAVSISGKAP--GSTTEGTGL
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LTSRFSVTDDLSLILGSRLINWKRDTSDRPYGGEETEVNREENGVFIPYAGVGYDLDDTW
                                                                                                                                                                                    TADDKACAVGLGTEIKQKALAF-----
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                                                                                                                                                                                                                                                              KFKMNSHD---VFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCN
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                                                                                                          NEQGRTTLYARGGLALNEFRSIPQVD------LIANARKGVRGYSHTVATENLDEFGIY
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                                                                                                                                                 -GSGLSQLPVRFSGTPRQDNLDLYATGPFSLFGREHELITGMTLSQYREN
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Pred. No. 2e-41;
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                                  GEGKTLHKASKTKFTGYAGAVYDLNDNN
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Wata Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasi DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AF2074
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AF2074
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A;Molecule type: DNA
A;Residues: 1-863 <KUR>
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               IVTEKNGDYSSFAVTVGTKIPASLREIPOSVSIITNOOVKDRNVDTFDOLARKTPGLRVL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLYASYTKIFNPQGAWVTDESNKPLDPMEGVGYELGIKGTHLNGKLNSSLAVFKLEQDNL
 GKFNTGSISHQILIGFDFNHNIDT:
                                                                                                                                                                                                                                                 GRVMAQTVGASPRPAEKNNRHETFYAAADWDI--NPDTVLGAGYLYQQRHLAPYNGLPAD
                                                                                                                                                                                                                                                                                  GPASVLFGAVEPGGIINVVTKQPLS--EPYYQLGFEVGNRAFYQPSIDFSGPLNADKTLL
                                                                                                                                                                                                                                                                                                      GPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGF--GTHKQYKAEADVSGSLNSDGSVR 212
                                                                                                                                                                                                                                                                                                                                                        DGADYNGSPAQDFIIRGFEQGGSFRNGYRDVNSYGLTGV-----GTI-----ERVEVLK 310
                                                                                                                                                                                                                                                                                                                                                                                       SNDDGRSS----VYARGYE-----YSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INOHLSASVNLNNVFDREYYSQSG---LYGVYGTPRNVMTSFKYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTNLPRNSFKTFTSYRLHGPLDKITIGGGVNWQSKV--GADLHTFSQGSYAVTNLMARYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLIMPKHSANLWTTYQV---TPELTIGGGVNAMSGITSSAGMHA---GGYATFDAMAAYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIWQHDN----VYSAEQDTTSKGIELELNGELAEGWQASAGYSY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGI
                                                                                                       SNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSR-----
                                                                                                                                                                           ANNKLP-----SLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDR-DAD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
                                   - PFRIGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVR
                                                                                                                                                                                                              YRFNASYQSSDGFQDFVNTNLTTIAPTIAWKLGDRTDLTLYYEYINFKGTFEQYTSILSD
                                                                                                                                        -NTFLPRSFYQAYPNNAYVDNTTQKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ferrichrome-iron receptor 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GB:BA000019; PIDN:BAB73847.1; ce: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.6%;
                                                                      -NAEEYTLATGVVNDQSLRQFAQDREFTQDNYFGQIDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 512; DB 2;
Pred. No. 1.3e-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
-----FARVVQRNVPNLD-IFNPNYNIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a synonym of
14-Dec-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PID:g17131239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anabaena sp. #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                            -GY-TLSHKFSDNWQIR
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, M.; Yasuda, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain PCC 7120
30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino-terminal homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Tabata, §
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434

GYSH---TVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE--

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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. B, 205-213, 2001
A;Title. Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:BA000019; PIDN:BAB73058.1; PID:g17130447; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                       GAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL----LMPKHSANLWTTYQVTPELTIG 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  734 -----QSGDLKGLGFGLGLYYVGDRYADVENTSLLSSYFRTDSAIYYKRDNWRLALNFRN 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 IFEVAAPTAPTPAQPESQVQPEQPS-----AESEEPIELVVTGEQDGYKVEDATGGTRT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYN 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 IDGLPAQMQSINGTLPNLFA-----FDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 KAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAEK-----N 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 NRHETFYAAADW--DINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADW 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKI 66
                        358 G-TEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEF
                                                   516 NPNYDVELPATPDESTFSY----TTRRDTLGIYVQDQITFADNLKLLVGGRFDAFQRKE
                                                                                                                                                                                                                 SGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT--NLDADGKLLKPRQGN
                                                                                                                                                                                                                                               571 EGFSETASEESLSAFSPRIGIVYQPIQAISLYASYSQSFKPDRFFGRSASNEPFKPTRGT
                                                                                                                                                                                                                                                                                                            OPEVGYKGSYMDDRLNARVSFYRMKDKNAAA--PLNPNNKKTRYAALGKRVMEGVETEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                   --- KLOINADN
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                                                                                                                      RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHY-KIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ferrichrome iron receptor [imported] - Nostoc sp. (strain PCC 7120)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647 GGVNAMSGITSSAGMHAGGYATFDAMAAYRFTPKL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   690 IFNRHYYARVGGANTFNIPGSERTWTANLRYSF
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A,Residues: 1-885 <KUR>
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C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-22001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2130
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E
DNA Res. 8, 205-213, 2001
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2130
A;Accession: AE2130
A;Accession: AE2130
A;Accession: AE20 cKUR>
A;Molecule type: DNA
A;Residues: 1-820 cKUR>
A;Cross-references: GB:BA000019; PIDN:BAB74295.1; PID:g17131689; GSPDB:GN00179
A;Gene: altrianary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 -AADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNKFKMNSHD 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVITWNISDRISLTFDLEYQDNDYLFDRGIPSIGDRPAP-IPISRFVGLP-HVYNDSTFR 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 TPVRDÍPGSIQVIPRÓILEDQKTTRIQEVLQNVSGVNKOGNYGGTD---AGGYRIRGFDQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGLPAQMQSING-----TLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
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562 SFDYGPRSSSTERFQTYGIYLQDQITFLDNLKLLIGGRPDMISGENTDNVTGDTTQNPDS 621
                                                                                                                      681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 AGLILAVESTTTATÖPPATPTSDAPPAEPIAQODDPIELVVTGEQDRYRVPTASTATKTD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATVLAALSSSVFAAQ----TADLETVHIKGQRS--YNAIVTEKNGDYSSFAVTVGTKIP 67
                                                                                                                                                                                                                                                                                              LNARVSFYRMKDKNAAAPLNPNNKKTRYAAL-----GKRVMEGVETEISGAVTPKWOIH
                                                                                                                                                                                                                                                                  AGYSYLHSQIKTASNSRDDGIFLL-MPKHSANLWTTYQVTPE----LTIGGG---VNAMS
                                                                                                                                                                                                                                                                                                                                                                                         GITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERT
                                                                       TKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDR
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12.9%; Score 486.5; DB 2; Length 820;
Best Local Similarity 24.6%; Pred. No. 7.1e-26;
Matches 185; Conservative 112; Mismatches 353; Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           714 WIANLRYSF 722
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A;Residues: 1-854 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73910.1; PID:g17131302; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                       Superfamily:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAA--PLNPNNKKTRYAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KILLGGREDIISQKQEDDNGETINFLQDEAFSPRIGLVYQPTKNISLYGSYSRSFTQVVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSS--VYARGYEYSEYNID 128
                                                                                                                         LAPIASTIPAPEQPEQPTSETPPAQPTAENNEPIELVVTGNQDQYRVEESSTATKIDAPL 216
                                                                                                                                                        LAALSSSVFAAQTADLETVH-----IKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AALNINNLFDTEYFETAFDALSV-VPGA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQINADNIFNRHYYARVGGANTFNIPGS 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGEQRSQGIELDIAGEILPGWKIIGGYAY--SDAKVTQDQEFEGNLLNNTPKHAFSLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL-LMPKHSANLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLIGGGRLG--HYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTN
GLRNGFKDFGFTSPRDVANIERVEFLKGPASVLYGSANNPGGVVNTITKKPLPDPSYRVG
                            GLPAQMQSINGTLPNLFA-FDRVEVMRGP-SGLFDSSGEMGGIVNLVRKRPTKAFQGHAA
                                                           RDIPASVOVIPKEIIODROVVRLNELANNVSGVQQQSGYGGLSSSGYFIRGF---ESGFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQVTPELTIGGGVNAMSGITSSAGMHAGG-----YATFDAMAAYRFTPKLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGL 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCNTADDKACAVGLGTEIK--QKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEPSFDKNDRQVYRLGYNFEHRFSENWQFRNSLRAAFQEYQNEAIFPLELL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NK--FKMNSHDVFA---DLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRP
                                                                                                                                                                                           183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - EDNRTLVRFAQSLESTRNVYVLNTNVVGDFKTGSIAHKLLFGFDLLRDDTRNRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ELQSGN----LQGLGFGLGLYYIGERQGDLSNSFELPSYFRTDAAMFYR-RNNFR
                                                                                                                                                                                                                                                   ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal
                                                                                                                                                                                         Conservative
                                                                                                                                                                                        12.8%; Score 483.5; DB 2; 24.1%; Pred. No. 1.2e-25; tive 134; Mismatches 328;
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                                                                                                                                                                                        Indels
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                                                                                                                                                                                             RGLELDIAGEILPGWKIIATYAYIDSSVSKDNDLERLNDRLSGV----PRNSASLWTTYE
                                                                                                                                                                                                                                                                                                                                             GKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVM
                                                                                                                                                                                                                                                                                                                                                                                                                                              R----LGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQ-TNLDAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFFSAPIASIDIFNPVYGAQPGTFDRSFAGEYGGDNL---AVYFQNLIEFTPNLKLLAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFRSIP--QVDL---IANARKGV--RGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTIGSYDFYRPTIDFTGPLTDDKSVLYRLNVAYENSGSFRDFIEN---ESFFISPVVTVN
INIKNLEDTEYYE---SQSFYLVPAAPLTVLGTISFEF
                                           INADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
                                                                                                                                               VTPELTIGGGVNAMSGITSSAGM----
                                                                                                                                                                                                                                           EGVETEISGAVTPKWQIHAGYSYLHSQIKTAS----NSRDDGIFLLMPKHSANLWTTYQ
                                                                                                                                                                                                                                                                                                                                                                                              RFDWIDSFDRDPVSNTVNNEVSESNFSPRVGIVYQPTNSTSLYASWTNSFNPQFFGRSRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISPKTSMTFEYEYQKYNYTFDRGLL--PGNTFFQIPISRFLGEPGFNNAEFISNVFTYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVG-ADWNKFKMNSHDVFADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGFGTHKQYKAEADVSGSLNSDGSVRGRV-MAQTVGASPRPAEKNNRHETFYAA--ADWD
                                                                                              FQK-----GSLAGLGFGLGLVYVDEREATLPNTIKIPSYVRTDASIFYR-RDNWRAA
                                                                                                                                                                                                                                                                                            GESFKPETSEQFEVGIKQEFFDKRLSATLAYFDITKNNVLTPDPVDNNFS---VQIGEQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYGKVGMRYSDRDADSNYAFAGSKL---GMKTPAGRPGCNTADDKACA
                                                                                                                                               -HAGGYATFDAMAAYRFTPKLKLQ
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A;Gene: all4924 C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor A;Experimental source: strain PCC C;Genetics: A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-858 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76623.1; PID:g17134062; GSPDB:GN00179 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AD2421 Nakazaki, N.; Shimpo, S. DNA Res. 8, 205-213, 2001 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, C;Species: Nostoc sp. A;Note: Nostoc sp. Strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence revision 14-Dec-2001 C;Accession: AD2421 AD2421 ferrichrome iron receptor [imported] - Nostoc sp. (strain PCC 7120) 17 VLAALSSSVFAAQTADLETVHIKGQ-----RSYNAIVTEKNGDYSSFAVTVGTKIPASL Similarity Conservative 127; 12.7%; Score 481; DB 2; 25.2%; Pred. No. 1.8e-25; Mismatches DB 2; Anabaena sp. strain PCC ' #text\_change 30-Jun-2002 Length 858; Indels S.; Watanabe, A.; , M.; Yasuda, M.; 96; amino-terminal Gaps 70 PCC 7120 27; Tabata, Iriguchi

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REIPQSVSIITNQQVKDRNVDTFDQLARKTPGLR-VLSNDDGRSSVYARGYEYSEYNI--LIVAVTSAKVAMQPP--ETPAIPEQPAAQPDEPIELVVTGEQDQYRVPAASVGTRTDTPL

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                                                       ISIAAVAGVAGLG----LAQAA-----VAGPDSADAAVTTANADDRSVSSVTIDAKRVA
                                                                                                                                                                 ---GTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGR---SSVY
                                                                                                                                                                                                                    DPSSSKFTAPLVDTPKSVTVIPAKIIEQTAATSLADILRTSPGIIFGAGEGGQPLADRPF
                                                                                                                                                                                                                                                                                                                              ARGYEYSEYN - - IDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR
                                                                                                                                                                                                                                                                                                                                                                                KRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASP-RPAEKNNRH
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    INMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSF-AVTV----
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A;Molecule type: DNA
A;Residues: 1-863 <KUR>
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D87252
TonB-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
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C;Accession: D87252
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 99, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Retaus: preliminary
A;Molecule type: DNA
A;Retaus: preliminary
A;Molecule type: DNA
A;Residues: 1-851 <STO>
A;Status: preliminary
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llarity 24.7%; Pred. No. 2.5e-25;
Conservative 126; Mismatches 341; Indels 138;
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Matches 198;
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A.Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C.Date: Id-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C.Accession: A12077 R.Accession: A12077 M.J. Takazawa, M.J. Yamada, M.J. Tabata, S. DNA Res. 8, 205-213, 2001 R.J. Takazawa, M.J. Yamada, M.J. Yasuda, M.J. Tabata, S. DNA Res. 9, 205-213, 2001 R.J. Takazawa, M.J. Yamada, M.J. Tabata, S. DNA Res. 9, 205-213, 2001 R.J. Takazawa, M.J. Yamada, M.J. Tabata, S. DNA Res. 9, 205-213, 2001 R.J. M.J. Takazawa, M.J. Yamada, M.J. Tabata, S. DNA Res. 9, 205-213, 2001 R.J. M.J. Takazawa, M.J. Yamada, M.J. Tabata, S. DNA Res. 9, 205-213, 2001 R.J. M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Yamada, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J. Takazawa, M.J.
ferrichrome iron receptor [imported] - Nostoc sp. (strain PCC 7120)
C.Species: Nostoc sp.
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RESULT 22
E64817
                     A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64817
A;Status. -----
                                                              probable membrane protein b0805 - Escherichia coli (strain K-12)

(;Species: Escherichia coli

(;Species: Escherichia coli

(;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

(;Accession: E64817

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; I

A; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.
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C;Superfamily:
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A;Experimental source;Genetics:
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nucleic acid sequence
e type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AA--PLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE--GKTLHKASKTKFTGYAGAVYDLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSL----PQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYS---DRDADSNYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSSGEMGGI VNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTV
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source: strain PCC
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ilarity 25.5%;
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C 7120
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Pred. No. 4.9e-25;
0; Mismatches 301;
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RESULT AC2140

23

737

INKSGYRYHPGEPRTFLLTANMHF

C;Species: Nostoc sp. strain PCC 7120 is a synonym of C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 C;Accession: AC2140

ferrichrome-iron receptor [imported] - Nostoc sp.

(strain

PCC

Anabaena sp. strain PCC #text\_change 30-Jun-2002

R; Kaneko,

Nakamura,

Y.; Wolk, C.P.; Kuritz, T.;

Sasamoto,

S.; Watanabe,

A.; Iriguchi

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A;Residues: 1-760 <BLAT>
A;Cross-references: GB.AE000182; GB:U00096; NID:g1787015; PIDN:AAC73892.1;
A;Experimental source: Krain K-12, substrain MG1655
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-tC;Keywords: transmembrane protein
C;Keywords: transmembrane protein
F;1-49/Region: tonB-box
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                                                                                                      NITPAWQVIGGYTQQKATİKNGKDVAQDGSSSLPYTPEHAFTLWSQYQATDDISVGAGAR
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VGGANTENI PGSERTW--TANLRY
                                                                      AMSGITSSAGMHAG-----
                                                                                                                                          AVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL--MPKHSANLWTTYQVTPELTIGGGVN
                                                                                                                                                                             NTSEIGTKWQVLDKRLLLTAALFRTDIENEV----EQNDDGTYSQYGKKRVEGYEISVAG
                                                                                                                                                                                                   NQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISG
                                                                                                                                                                                                                                                                                                                           AIYAFDTLQITRDFELNGGIRLDNYHTEYDSATACGGSGRGAITCPTGVAKGSPVTTVDT
                                                                                                                                                                                                                                                                                                                                                              GIYGKSTFHPADGLSLIGGGRLGHYKIE------
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                                   YI-----GSMHKGSDGAVGTPAFTEGYWVADAKLGYRVNRNLDFQLNVYNLFDTDYVAS
                                                                                                                                                                                                                                                  AKSGNLMNWKAGALYHLTENGNVYINYAVSQQPPGGNNFALAQSGSGNSANRTDFKPQKA
                                                                                                                                                                                                                                                                                     ASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTPQ-----TNLDADGKLLKPRQG
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Pred. No. 9e-25;
                                                                      -GYATFDAMAAYRFTPKLKLQINADNIFNRHYYAR
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A; Fitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Recession: AC2140
A; Accession: AC2140
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-867 < KUR>
A; Residues: 1-867 < KUR>
A; Experimental source: strain PCC 7120
C; Genetics: A; GSPDB:GN00179
C; Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----RGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLV 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NYAFAGSKLGMKTPAGR----PGCNTADDKACAVGL---GTEIKQ-------KALAFDA 370
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 867;
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.4%; Score 467.5; DB 2; Best Local Similarity 24.7%; Pred. No. 1.6e-24; Matches 186; Conservative 127; Mismatches 264;
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RESULT 24 S74450

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ferrichrome-iron receptor 2 - Synechocystis sp. (strain PCC 6803)

N;Alternate names: protein sll1406
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S74450
C;Accession: S74450
C;Accession: S7450
O; K.; Okumura, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: fhuA 2
A;Start codon: GTG
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
                                                                                                                                                                                                                                                                                                                                                                                                                                              NID:g1651650; PIDN:BAA16602.1; PID:g165167
to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: iron transport
F;213-346/Domain: tonB-dependent receptor amino-terminal homology <TNN>
F;547-828/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGAD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 ADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEF-----VIGADYNRFRSTN 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLAALSSSVFAA---QTADLETVHIKGQRSYNAIVTEKNGDYSSF--AVTVGTKIPASLR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DGLPAQ-MQSINGTLPNLPAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQGRITLYARGGLALNEFRSIPQVDLIANARKGVRGYSHT---VATE-----NLDBFGIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.3%; Score 465; DB 2; Length 828; Best Local Similarity 23.1%; Pred. No. 2.3e-24; Matches 182; Conservative 119; Mismatches 303; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                  ahown
                                                                                                                                                                                                                                                                                                               A;Accession: $74450
A;Status: nucleic acid sequence not shown; translation not
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                         A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Cross-references: EMBL:D90899; GB:AB001339; A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 HAAAGFGTHKQYKAEADVSG-----
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PRISANLIWITYOUTPELTIGGGVNAMSGITSSAGMHAG	KQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARG	
PRINCESIANTWEIT	GNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEI	
PKHSANLWTTYOUTPELITICGGVNAMSGITSSAGMHAG	-VLGAGYLYQQRHLAPYN-GLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYF 	
PKHSANLWTTYOUTPELLTIGGGVNAMAGGITSSAGMHAG	THKQYKAEADVSGSLNSDGSVRGRVMAQT-VGASPRPAEKNNRHETFYAAADWDINPDT	
PSNOPSLATIVELITIGGGVNAMSGITSSAGMHAG	MQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFG  :    :   :    :    :    :    :    :	
PSNQFSLWTTYELTIGGGVNAMSGITSSAGMHAG	VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY-EYSEYNIDGLPAQ : :    :: :     ::      :: :     :::   :::     :::   ::	
	VLAALSSSVFAAQTADLETVHIKGORSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQS    ;	
	<pre>itch 12.2%; Score 460.5; DB 2; Length 851; sal Similarity 23.6%; Pred. No. 4.9e-24; 173; Conservative 120; Mismatches 316; Indels 123; Gaps</pre>	
PSHQPSLWTTYQUTPELTIGGGVNAMSGITSSAGMHAG	equence of the Filamentous Nitrogen-fixing CyanobacteriumUID:21595285; PMID:11759840  0019; PIDN:BAB74287.1; PID:g17131681; GSPDB:GN00179 in PCC 7120  iron receptor 1; tonB-dependent receptor amino-terminal	
616 NSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG 717 TDIVDNTLSNVPSNQFSLWTTYEI	<pre>imported] - Nostoc sp. (strain PCC 7120) CC 7120 is a synonym of Anabaena sp. strain PCC 7120 ce_revision 14-Dec-2001 #text_change 30-Jun-2002 Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.;</pre>	
616 NSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG 717 TDIVDNTLSNVPSNQFSLWTTYEIQSGNLQGLGFGLGLFYVDQREGDL 665GYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTW	TANLRYSF : :   VGKIGVTF	
616 NSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAG	gyatedamaayreteklklqinadnienrhyyarvggantenipgsertw 	
	NSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMHAGTDIVDNTLSNVPSNQFSLWTTYEIQSGNLQGLGFGLGLFYVDQREGDL	

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8	B &	₽ 5	\$ B \$	D Q	ДУ	Db 97	Que Bes Mat	A; Sta A; Res A; Crc A; Crc A; Exr C; Ger C; Sur	R;Hay gasav DNA F A;Tit A;Ref	RESUI C9073 hypot C;Spe C;Dat	D 42	ф	Ş	D Q	Db Qy	В
yy 391 ynrfrstneggrttlyargglalnefrsipqudlianarkgvrgyshtvatenl 	Y 335 GMKTPAGRPGCNTADDKACAVGLGTEIKOKALAFDASYSRPFRLGNTANBFVIGAD :	278 LECHVEVGADWNK :         : 290 VDTHNFYGTDSDY	233	179 KAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQ 	Y 120 YEYS-EVNIDGLÞAQMQSINGTĽÞNLFAFDRVEVMRGÞSGLFDSSGEMGGIVNLVRKRÞT		Query Match 12.2%; Score 460; DB 2; 1 Best Local Similarity 22.6%; Pred. No. 4.5e-24; Matches 168; Conservative 109; Mismatches 333;	Accession: C90739 Status: preliminary Molecule type: DNA Molecule type: DNA Residues: 1-760 <hay> Cross-references: GB:BA000007; PIDN:BAB34306.1; PID Experimental source: strain O157:H7, substrain RIMD Genetics: Genetics: Gene: EC90883 Superfamily: ferrichrome-iron receptor 1; tonB-depe</hay>	Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, Asawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T. NA Res. 8, 11-22, 2001 NA Res. 6, 11-22, 2001 Fille: Complete genome sequence of enterohemorr Reference number: A99629; MUID:21156231; PMID:1	rotein ECs0883 [imported] - Escherich herichia coli -2001 #sequence_revision 18-Jul-2001 90739	27 684 QIXADNIFNKHY 695 b 814 GLNFKNIFDVNY 825	765QSC	642 ELTIGGGVNAMSGITSSAGMHAG	YY 583 MEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL-LMPKHSANLWTTYQVTP  : : : :  ::   ::	527 LKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAP :: :  :  :  :  :: :: ::    654 IEPERGTQYEVGVRGEFLDGKLIASLAGYQITKTNVATPDPAD	594 DETNOSELSIVDGVKFEDISDQAFSPRIGIVYQPITPLSLYASYSRSFAQNEGIQRDNSR
GVRGYSHTVATENLDEF 447	RPFRLGNTANEFVIGAD 390   : : :   :   STFYTASIGHDVSTGVE 399	NYAFAGSKL 33	ADANNKLPS 27	TVGASPRÞÆKNINHETFYA 238 	SSGEMGGIVNLVRKRPT 178                 GRSAPTGSINMISKQPR 178	SNDDGRSSVYARG 119 : :    :      AGENGNSTIGDAIYMRG 122	Length 760; Indels 134; Gaps 23;	:g13360342; GSPDB:GN00154 ) 0509952 ;ndent receptor amino-terminal homol	K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Hattori, M.; Shinagawa, H. hagic Escherichia coli O157:H7 and geno 1258796	ia coli (strain O157:H7, substrain RI #text_change 24-Aug-2001		TRTDAALFYR-RDNWNI 813	GYATFDAMAAYRFTPKLKL 683	LMPKHSANLWTTYQVTP 641   :  :   :    RVPENSASIWTTYEL 764	LNPNNKKTRYAALGKRV 582 	YSRSFAQNFGIQRDNSR 653

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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho.
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83043
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C;Genetics:
A;Gene: PA4837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 1:Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: A83043
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable outer membrane protein PA4837 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                      567 NTSEIGTKWOVLDKRLLLTAALFRTDIENBV----EQNDDGTYSQYGKKRVEGYEISVAG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 QSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQ 194
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                                                                                                                                   -KTLHK 484
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Best Local Similarity 22.7%; Pred. No. 4.8e-24;
Matches 172; Conservative 135; Mismatches 329; Indels 122; Gaps
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                          391 YNRFRSTNEQGRTTLYARGGL---ALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEF
                                                                   400 FTRETQTN:----YGVNPVTLPAVNIYHPDSSIHPGGLTRNGANANGQT-----DTF
                                                                                                                                                                                           447 AIYAFDTLQITRDFELNGGIRLDNYHTEYDSATACGGSGRGAITCPAGVAKGSPVTTVDT
                                                                                                                                                                                                                                                   ASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTPQ------TNLDADGKLLKPRQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 593 AVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLL--MPKHSANLWTTYQVTPELTIGGGVN
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                                                                                                                                      GIYGKSTFHPADGLSLIGGGRLGHYKIE
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A;Residues: 1-708 <STO>
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E85589
hypothetical protein Z1026 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Species: Escherichia coli
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R;Pecna, N.T.; Punkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller; L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Reference number: A85480
A;Reterence number: B85880
A;Reterence number: B85880
A;Reterence number: B85880
A;Reterence number: B85880
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A;Reterence number: B1008
A;Reterence de number: B1008
A;Reterence number: B1008
C;Generica: B1008
C;Generica: B1008
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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                                        592
                                                                                                                                                                                                                                                                                622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 YEYS-EYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPT 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 AADWDINPDTVLGAG-----YLYQQRHLAPYNGLP------ADANNKLPS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GMKTPAGRPG----CNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGAD 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 KIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGL-RVLSNDDGRS----SVYARG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNY---AFAGSKL 334
--KTLHK 484
                                                                                                               --TNLDADGKLLKPRQG
                                                                                                                                                                                                                                                           AKSGNLVNWKAGALYHLTENGNVYINYAVSQQPPGGNNFALAQSGSGNSANRTDFKPQKA
                                                                                                                                                                                                                     NQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISG
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                                                                                                               ASKTKFTGY-AGAVYDLNDNNSLYLSLSQLYTPQ-
  GIYGKSTFHPADGLSLIGGGRLGHYKIE-
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PTKAFQ-	YEYSEYNI :::::: FQATQTGVFL	[PASL]	SVFRI     ;   RLAL	7	ypelminary yper 1-747 <kur> 1-747 <kur> yrences: GB: C 718 C 718</kur></kur>	Seq nber: 97408	odner, B.; Hinkle, ( Liu, F.; Wollam, C nce 294, 2323-2328,	2001	51401	NLFDR	YEFR	: TYQYT	ALGK  - AGE	GTDM	JVRFD	SLIGGGRLGHY-	SIPO	COKAL	RHHF	: :	LVEA
. D	FLDGL	REIPQ :   -  KAIPQ	NATAA   GTAAV	rity	DNA 7 <kur> es: GB:A</kur>	ience A973	le, G n, C. 328,	#seq	(imp	HYAR HHH RYYER	SGWLH	PELTI	RVMEG  - ARSQG	AGKAF	RYRQD	XE	/DLIA ; RNPYA	SWHDS	VEQWS	SNGGY	EVVRN
:   -:	PAQMQ	SVSII	TVLAA :: VLMGP	11.9%; illarity 25.0%; Conservative 10	GB:AE007869;		G.; Ga C.; All , 2001	uence	orted	VGGAN	GADAG	NLWTTYQVTPELTIGGGVNA-	VETEI ; ; FDLQF	DBBBG  -:-	MNATR	<del>K</del>	-NARK :  : IDIRR	GTEIKQKALAFDASYSR   : :   :: RREYRYRDFEWHDSITQLDL	LRLAS	GKVGM ::	RQVFD
GHAAAGF-  :	SINGT   GFGGF	TNQQV   : : GRQEM	VMG	9%; 0%; 104	0	he Pl MID:1	G.; Gattung, C.; Allinger, 2001	_revision		TENTP	AAVNY	A	SGAVT    :  SGQLT	RGYEA	: :  LNNGR	IESGE	LNEFRSIPQVDLIA-NARKGVRGY        :   :   :   LRSIPSRNPYAIDIRRPVYGQPKP	TLGDT	нукна	RYSDR 	PDTSLLVEAEVVRNRQVFDRGTVAPH-
	LPNLF ; ; QMDAY	KDRN-	FAAQT   :  HAQET	Score Pred. ; Mi	IDN:A	ant P 17431	35.00	ä	groba	GEPRN	VGERA	: SW	PKWQI: : :: EQLRL	GVKTD	FRETS	-GKTL	PKPPF	RIGNT	HLD-G	DADSN	PH
GT	DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKR 	VGTKIPASLREIPQSVSIITNQQVKDRN-VDTFDQLARKTPGLRVLSNDDGRSSVYAR 	GQFMSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVT	; Score 450.5; ; Pred. No. 2e- 104; Mismatches	PIDN:AAK86224.	the Plant Pathogen PMID:11743194	Miller, N Doughty,	30-Sep-2001	Agrobacterium	INDIVITENT FOR THE TANKY SET OF THE TANK	SLMGVYEFREGWLHGADAGAAVNYVGERAGDSSDSGFELPAYTTVDLLARYPLASNATLG	-MSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQ	KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA     -     -     -     -  -  -  -  -  -	YIPQINLDAUGKLIKPRQGNQFEVGYKGSYMDUKUNAKVSFYKMKUKNAAAPLNPNNK :	: :     :   :   :   :   :   :   :   :	-KIESGE-GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQL	FRSIPQVDLIA-NARKGVRGYSHTVA	GTE KQKALAFDASYSKPFRLGNTANEFYIGADYNRFRSTNEQGRTTLYARGGLA   : :   :   :     RREYRYRDFEWHDSITQLDLLGDLHTGSIRHQLLMGLEYERYHNDELI	LQATLRHHFNEQWSLRLASHYKHGHLD-GYASENSSLA	VFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGL	
GTHKQYKAEADVSGSLN-SDGS-	EVMRG   ::  EVLKG	QLARK ::   EVLRY	VHIKG : ::  ITVEG	22.	24.1;	en and	er, N.; hty, D.	0-200			SGFEL	AGMHAO	YLHSQ:	LGMTLA	RAATPI	rketg:	SHTVATENLDEFGIYGKSTFHPADGL	GADY	SSLA-	SKLGMI	-NHLGSLPRSRFFGEPDDGKIDNNNET
AEADV: 	PSGLFI  : : PASVL	FPGLR	QRSYNI   ;    QAENI	)B 2; 358;	PID:		.; B1; D.; S	1 #text	tumefaciens	708	PAYTT	GYATI	IKTASI ; VTKDEI	SFYKMI : : :	RIGVL:	YAGAV	TENLDI   ;	NRFRS	-	KTPAGI	LPRSRI
SGSLN	)SSGEI	VLSI	AIVTE	Length Indels	PID:g15155326	Biotechnology	Blanchard, I; Scott, C.;				/DLLAI	- LAMAD	NSRDDO       ARGS		/ /QATPI	/DLNDI	EFGIYO	NEQGI	1	RPGCN.	FGEPI
-SDGS :	AGGIV	NDDGR       DPDT	KNGDY.	-1	5326;	ology	~ ~	change	(strain		RÝPLA	AYRFT	GIFLLI   SRLLN	-AAAP	: EVGLF	NNSLY	GKSTFI ; LQDQI:	RTTLY		PADDK	DDGKI
VRGR :	IVNLVRKR    ;     IVQMVSKR	SSVYAJ    DWFYIJ	TEKNGDYSSFAVT   ; TGPVRGYVAKKSA	••	GSPDI	Agent	M.; Qur ; Lappas	11-Jan-2002	in C58,		SNATL		MPKHSI :	SNPGY	NASK	rostst	TENLDEFGIYGKSTFHPADGL   ;   ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	ARGGLA	ADGYSL	ACAVGI	NNNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259
686 NTLRVSDAAVFDAAIRYE-KNDWTASVNVANVFDKEYVKSCAGVSVCGW-GDSRTITLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 LPSLPQHVFVG-ADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 AQDTPVRETEIGINNFGNAFFGFDLGDKVDAEGVWK-YRVTGKVSGGDNYTDYSEDLRGF
                                                                                                                                                                                                          DALSGRAGIAYEFDNGLTPYVSAATFENPLIDTLADGTPASPEEGHQFEAGIKYEPSFFD
                                                                                                                                                                                                                                                                               THEVYADNIVIO--QQIGIYAQDQLREGDGWLVTLNGRYDYVDTELNNRLPAGVSRRSND
                                                                 YTDLDITKDANPNLIGKSPWIVPAHTASLWVDYAFTDETFEGLSIGGGVRYQGKSWADAA
                                                                                                                                        GSITASV-FKLVKD-NAIVSYTAGGVTTS-GQFGQVESTGFELEAKANLDENWKALASYS
                                                                                                                                                                         DRINARVSFYRMKDKNAAAPINPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYS
                                                                                                                                                                                                                                                                                                                ----YSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE---GKTLHKASK 487
                                                                                                                                                                                                                                                                                                                                                   GAVNHSPLFGLDYKYYRLDQVQACCGSNAIGAL----
                                                                                                                                                                                                                                                                                                                                                                                     GNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRG---- 434
                                                                                                                                                                                                                                                                                                                                                                                                                        FGKLDRKAFYGEPDIDNGRVYQSMVGYDVSHEFDNGWKISQNARYGHLYKHETGPYPGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPQ-ITFEP-DAQTSATLYGYFSALD-----QVHVGNGFL------PYVGTVVDA--P 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VMAQTVGASPRPAEKNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNK 274
                               AGMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANL
                                                                                                    YLHSQIKTASNSRDDGIF-LLMPKHSANLWTTYQVTPE----LTIGGGV--NAMSGITSS
                                                                                                                                                                                                                                             TKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVG--YKGSYMD
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TonB-dependent receptor [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plas (;Species: Agrobacterium tumefaciens (;Pate: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002 (;Accession: A13197 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Lerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-3323, 2001 ; Karp, P.; Romero, P.; Bang, S. Science 294, 2317-323, 2001 ster, E.W. Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, P.; Pittle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; PMID:11743193 A;Reference number: AB2577; PMID:11743193 A;Reference number: AB2577; PMID:11743193

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-819 < KUR> A;Cross-references: GB:AE008687; PIDN:AAL45999.1; PID:g17743754; GSPDB:GN00188 A;Experimental source: strain C58 (Dupont)

C;Genetics: A;Gene: Atu5311

A;Genome: plasmid

Ś 밁 Š Query Match

Best Local Similarity 25.5%; Pr
Matches 187; Conservative 106; 134 33 LETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDT 92 93 LQTITVQGAESAYGHV---DGIVASRSAT-GTKTDTPLIEVPQSISVITADEVKARGAET 189 Score 450; DB 2; Length 819; Pred. No. 2.5e-23; D6; Mismatches 349; Indels 92; Gaps

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ferrichrome iron receptor Atu0409 [imported] - Agrobacterium tumefaciens (strain C58, Duj C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 [SAccession: AH3626 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. Frwod, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, D.
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Afitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8
A,Reference number: AB2577; PMID:11743193
A,Accession: AH2626
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A.Residues: 1-708 <KUR>
A.Cross-references: GB:AE008688; PIDN:AAL41430.1; PID:g17738752; GSPDB:GN00186
A.Experimental source: strain C58 (Dupont)
                                                                                  ----DIFDQLARKTPGLRVLSNDDG-RSSVYARGYEYSEYNIDGLPAQMQSINGTLPNLF 145
                                                                                                                                                                                              TLQFDYLNDER---PFDRGFLAFGEGIIDT-PLERFFGEPDDVRKVEEIGLSYRLEHNFN 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : | | : | | : | | : | DIWKIRNAFRYQSSDT-FDYRAEPVRLNETTGILTRNFRSNDDYEENYTLQTDVVGK--- 524
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                                                                                                                                                                                                                                                                                                                                       VLGAGYLYQQRHLAPYN-GLPADANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFG 307
                                                                                                                                                                                                                                                                                                                                                                                                                       NGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----FITGSINHTLLFGVDLARFTSGGTQSRLP-----GVITPSINVFNPVYNAIP 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFEVGYKGSYMDDRLNARVSFYRMKDKNAAAP--LNPNNKKTRYAALGKRVMEGVETEIS 591
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                          146 AFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSL
                                                                                                                                                                                                                                                                                 | | | :: |: | : | : | : | 367 NSDKTLLYRL-----NSVYETSDGFRDFNQDVQRFFISPTLKWEIGKAINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - POVDLIANARKGVRGYSHTVATENLDE - - - FGIYGKSTFHPADGLSLIGGGRLGHYKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 GLFYVGDRQGDSSNTYI-IPGYLRTDA-AIYYKRDNWRAGINIQNLFNEKHYL---GANF
                                                                                                              266 GGFGSTSDQ1-----GIRGFFGDGTFGGSILVDGFK-----DGRGGIRETAN-----
  IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNV
                                                                                                                                                                                                                                                       NSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAAD----
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C;Species: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp.
C;Stecies: Nostoc sp.
C;Stecies: Nostoc sp.
C;Stecies: Nostoc sp.
C;Accession: AC2134
C;Accession: AC2134
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8 206-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2134
A;Accession: AC2134
A;Accession: AC2134
A;Accession: AC2134
A;Accession: AC2134
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alt2626
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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                                                                              QIDPYLLERIEVLKGPSSVLYGQNYPGGMINMVSKRPTDKPFNEVVAGTGT-----DGR 296
                                                                                                                                                     |: : | | | : : | | | : : | 297 AYGAFDFSGPVAGNDAFLYRLTGVATRTGTNIDYTKDERFMLAPSFALKPDEDTTFFLS 356
                                                                                                                                                                                                                                          190 IKEAVNYTAGVHV-----GGSSASTRAFDNIE--IRGFAPTPLYLDGTYLPYIGDLGGSP 242
                                         ----FAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEAD 200
                                                                                                                                                                                                                                                                                                GYGKVGMRYSDRDADSNYAFAGS--KLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALA 367
                                                                                                                                                                                                                                                                                                                            117 WSIRHNAKYISVDDSYRTFFSGGYVETGGVTDYTKMRRNAIDYSS------NNQVFA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 DDRLNARVSFYRMKDKNAAAAPLNPNNKKTRY--AALGKRVMEGVETEISGAVTPKWQIHA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA-GMHAGGYATFDAMAAYRF---TPK---LKLQINADNIFNRHYYARVGGANTFN--IP 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGE---GKTLHK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 ASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYM 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQV----TPELTIGGGV-NAMSGITS 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                           VSGSLNSDGSVRGR--VMAQTVGASPRPAEK--NNRHETFYAAADWDINPDTVLGAGYL-
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llarity 24.2%; Pred. No. 3e-23;
Conservative 120; Mismatches 303; Indels 139;
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C; Genetics:
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A; Map position:
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D83081
                                                                                                          probable outer membrane receptor for iron transport PA4514 [imported] - Pseudomonas C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 14-Sep-2001 C;Accession: D83081
                                      R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, .; Lory, S.; Olson, M.V.; Lory, S.; Olson, M.V.; Nature 406, 959-964, 2000
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Complete genome sequence of Pseudomonas aeruginosa PA01, nce number: A82950; MUID:20437337; PMID:10984043
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K.; Lim,
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A;Accession: D83081
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-753 <STO>
A;Residues: 1-753 <STO>
A;Cross-references: GB:AE004865; GB:AE004091; NID:g9950752; PIDN:AAG07902.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA4514
C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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DKRYFDQVYSTHMAHVAPG--RTALLGVNFHF
                                                                                                                                DGEQRVQGVELGENGKLTEKWKVFGGYTYLDSEIRKSTVKSDEG--NKMPQTAQNNFTLW
                                                                                                                                                               LGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSAN---LW
                                                                                                                                                                                                ADISVGNNGLDPERNRNLELGTKWAFFDDALSLNAALFR-TDKTNARVASP-DVSTLQVL
                                                                                                                                                                                                                                 TNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAA
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                                NRHYYARVGGANTENI - PGSERTWTANLRYSF
                                                                TTYDLLQNFTIGGGTTYVDKQYGNTANS-TYIPSYWRYDAMASYKVSKNVDLQLNVQNLT
                                                                                                 TTYQVTPELTIGGG----VNAMSGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIF
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22.9%;
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probable TonB-dependent receptor PA1322 [imported] - Pseudomonas aeruginosa (strain PAO1 C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Dseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 14-Sep-2001 C; Accession: A343481
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ... Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathor A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Recence number: A82950; MUID:20437337; PMID:10984043
A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Status: L-722 csTC>
A; Cross-references: GB:AE004561; GB:AE004091; NID:g9947253; PIDN:AAG04711.1; GSPDB:GN001
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA1322
C; Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol
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ferrichrome-iron receptor [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Noce: Nostoc sp.
A;Noce: Nostoc sp.
A;Noce: Nostoc sp.
C;Accession: AE2081
C;Accession: AE2085
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Cross-references: GB:BA000019; PIDN:BAB73935.1; PID:g17131327; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 IVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVL 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 SKLGMKTPAGRPGCNTADDKACAVGL-GTEIKQKALAFDASYSRPFRLGNTANEFVIGAD 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 NAAYENARSFRDFVEN--ESTFIAPIITVKAGERTNLTFGYEYOKYDYTFERGFP--SNN 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLP-SLPQHVFVG-ADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAG 331
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11.2%; Score 424; DB 2; L. ilarity 23.8%; Pred. No. 1.8e-21; Conservative 124; Mismatches 328;
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Best Local Similarity
Matches 170; Conserva
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A; Status: preliminary
A; Molecule type: DNA
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <PAR>
A;Cross-references: GB:Al
C;Genetics:
A;Gene: STY0396
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Nature 413, 848-852, 2001
A;Authors: Parry
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A;Accession: AC0547
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YAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLW
                                                               TSTSFADENGNVLEPMKGKQWEAGVKYEPLGGNSQFSAAVYRINQTNIATKEEPTDP---
                                                                                                                         TPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTR
                                                                                                                                                                                     DRWRFTLGGRYDRVSVSNID--KLHDSRSDLDKNNVSTRAALLYLFDNGVAPYLSYSTAF
                                                                                                                                                                                                                                               DGLSLIGGGRLGHYKIESGEGKTLHKA----SKTKFTGYAGAVYDLNDNNSLYLSLSQLY
                                                                                                                                                                                                                                                                                                        NHTTGY-----YGAFPPIDAFNPVYGAQPDYITLYSREKHKLRQTGYYLQDQM-SW
                                                                                                                                                                                                                                                                                                                                                                  GRTTLYARGGLALNEFRSIPOVDLIANARKGVRGYSHTVATE--NLDEFGIYGKSTFHPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQ 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FFEGEDDYDKYDRRENMVGYNIEHLFDNGWSVRQKLRYLHTKVTLNQVYAAGWLN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFVGA-DWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALMPSITWRITDRTRLDLMAYLHRDPQGGSHSGLPYQGTVVPYNG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFYAAADWDINPDTVLG-AGYLYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKPAFDAGGEVKLFAGNNNORGAAFDVTGPLDDNERVAARLSGMTRYADSOFTPLKEERY 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSDGSLDNVYLDGLKMMGDTNSHSSLVVDPWFLEDIEVVRGPASVLYGRSSPGGIVSLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEYSEYN----IDGLP---AQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRLATPDIETPOSVSIITROOFEEQGATSVROAVSYTPG--VYSNOIGASNRFDYIVLRG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKIPASLREIPOSVSIITNOOVKDRNVDTFDQLARKTPGLRVLSNDDGRSS----VYARG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MFATTRMALLIGGAIGGATFPLFAQETTKNDTV-----IVT-----SPVQSGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTAATVLAAL-----SSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDASIFYK-RDNWRAALNFKNLFDTKYYE---SQSFFIVPAAPFTVLGTVSFEF
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Pred. No. 2e-21;
1; Mismatches 353;
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ple drug resistant
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Salmonella enterica s
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, L.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  828
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A;Residues: 1-853 <KUR>
A;Cross references: GB:BA000019; PIDN:BAB73884.1;
A;Crosental source: strain PCC 7120
C;Genetics:
A;Gene: alr2185
C;Superfamily: ferrichrome-iron receptor 1; tonB-d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: Nostoc sp. strain PCC 7120 is a synonym of j
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #
C;Accession: AC2079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.D.; Kuritz, T.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, N
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AC2079
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DNA Res. 8, 205-213, 2001
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Best Local Similarity
588
                                   417
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                                                                                                                                               GILTRTYAOR------EYKSDDYSLOTNVVGKFTTGSIKHTLLAGVDFN
                                                                                                                                                                                    KLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSTNAFIGNOITIRGFSTSNLPILRDGFRIYE---NFSFQETSNLERIEVLKGPASVQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSNDDGRSSVYARGYEYSEYNI - - DGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVVTGEKDGYQVPNTATV-TRTNTPIIDIPQSIQVVPRQVLEDQQITRVDDALRNVPGVL
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                                 RSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIES
                                                                        RGLLDDLVFRGTRTTLNIFNPVYGVPPRTDFSTLPPATPFKNETTRLGFYLQDQIALNN-
                                                                                                                                                                                                                        PYSRVFNDPD-DFIDTKSFSIAYNLEHRFSDNWTLRNSFRYLQQDLFTQATLAGSLNETT
                                                                                                                                                                                                                                                             P-QHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGS-----
                                                                                                                                                                                                                                                                                                                                        SPRPAEKNNRHETFYAAAD--WDINPDTVL--GAGYLYQQRHLAPYNGLPADANNKLPSL
                                                                                                                                                                                                                                                                                                                                                                             QLDPGGVINLVTKKPLSEPFYEIQAQFGSYGLIRPSFDVSGPLTDDGKLLYRLNA-TYQR
                                                                                                                                                                                                                                                                                                                                                                                                               SGEMGGI VNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIVT-EKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLR 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFMSVFRINMTAATVL--AALSSS----VF--AAQTADL----ETVHIKGQRSYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YRSIGEIESKGVELEAISHLSDSVRLQAAYTYTDIRYKKSSPQEQGKRAVYAPRNQASAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 420.5; DB 2; 23.1%; Pred. No. 3.1e-21;
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 SAWSPVIGL
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                                                                                                            -NEOGRITLYARGGLALNEF
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#text_change
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M.; Yamada, M.; Yasuda, M.; Tabata, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 177;
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30-Jun-2002
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homol

Ana

QFTVLAGLRYDTVDFKDTFTDESKYD---

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C;Species: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp.
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: Ac2132
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Realdudes: L857 «CMS)
A;Crosa-references: GB:BA000019; PIDN:BAB74309.1; PID:g17131703; GSPDB:GN00179
A;Experimental source: strain PCC 7120
MNSHDVFADLKHYFGNG----GYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTA 348
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A; Accession: GRBL.
A; Coss. references: EMBL.D90899; GB: AB001339; NID: G1651650; PIDN: BAA16609.1; PID: G165168
A; Coss. references: EMBL.D90899; GB: AB001339; NID: G1651650; PIDN: BAA16609.1; PID: G165168
A; Molec: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Conetics:
A; Genetics:
C; Acperticanily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homology
C; Keywords: iron transport
F; 241-371/Domain: tonB-dependent receptor amino-terminal homology <TNN>
F; 579-853/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
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Retrichmone-iron receptor 3 - Synechocystis sp. (strain PCC 6803)

N,Alternate names: protein slr1490

C;Species: Synechocystis sp.

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: 874457

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

R;Kokuntra, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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                                                     663 VGIKAELLQGNLFATLAYFDITKQNVST-ADPDVLGAS-VATGEQRSRGIELSAVGTIAP
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GEGKTIHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPROGNQFE
                                                                                                                                                                                        VGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         700 GGANTFN----IPGSERTWIANLRYSF 722
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Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Iheaultr, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: C95382
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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A; Residues: 1-714 < KUR>
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                                                                A;Genome: plasmid
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   110;
                  Score 411; DB 2;
Pred. No. 1.1e-20;
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Mismatches
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                               Length 714;
   Indels
   120;
 Gaps
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N.A.; Fisher, R.F.
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                                              LQINADNIFN-RHYYARVGGANTFNIPGSERTWTANLRYSF
FQLNVNNLFDEXHVASKDSGAVYYN-PG--RSILATLRQSW
                                                                                             SVWGTYTLEGDGARGDMLFGLGARYTDAYYTSITNTTSSESA--VVFDAAFTYKIQENTT
                                                                                                                                         NLWITYQVIPELTIGG---
                                                                                                                                                                                            KVRH---
                                                                                                                                                                                                                                                                                                                                                                                  SFGLRNDWLDLSETNLLAG---TRRAGNHREFTTRIGASYKVTEELAPYISYAESAAP--
                                                                                                                                                                                                                                                                                                                                                                                                                              IGGGR-----LGHYKIESGEGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQT
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                                                                                                                                                                                                                                    KTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSA
                                                                                                                                                                                                                                                                                     --PAAGS--DPTTGKQYEVGIK--YRPDAFPAMFTASVYDLTKGNITVFDQVTYLPQTVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAF
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                                                                                                                                                                                          ---RGFELEAKAEVTNNISVIAAYSYIDSKIEEPGGANDGNRLMRVPKNMA
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C;Pare: C;Pares C81861
C;Accession: C81861
R;Parkhill, J.; Achtman, M.; James,
R;Parkhill, J.; Jagels, K.; Leather, A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: C81861 A; Experimental source: C; Genetics: A;Status: preliminary A;Molecule type: DNA A;Residuss: 1-635 <PAR> A;Cross-references: GB:AL162756; ; Holroyd, S.; Jagels, K. Nature 404, 502-506, 2000 hypothetical protein NMA1663 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-20 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-20 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-20 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-20 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-20 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-20 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-20 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #seque serogroup GB:AL157959; NID:g7380091; PIDN:CAB84891.1; A, strain Z2491 K.D.; Bentley,
S.; Moule, S.; S.D.; Churcher, Mungall, K.; Qu #text\_change 02-Feb-2001 Neisseria menigitidis Z2491 er, C.; Klee, Quail, M.A.; Z2491 PID: 9738030 S.R.; Morel Rajandream, serogroup

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Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol

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                                                                                                                                                                                                                                   201 IRKRPTASFK-HTGELTADHRGSRRAVLDVSGSLNKANTLRGRL----VGABEYKKSFKD 255
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                                                                                                                                                                                                                                                                                           RVWGRKHMVYGIAEADAGDSSVLTLGGMYQKSREVPDFSGIILSCENQKTAPFSSTP--A 313
                                                                                                                                                                                                                                                                                                                                                       366
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                                                                                                                                                                                                                                                                                                                                                                                                                                  388 GAD---YNRFRSTN-EQGRITLYARGGLALNEFRSIP-QVDLIANARKGVRGYSHTVATE 442
                                                                                                           TVGTKIPASLREIPOSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGY 120
                                                                                                                                                                                                                                                                       ---NRHETFYAAADWDINPDTVLGAGYLYQQ------RHLAPYNGLPADA 271
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                             Gaps
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                                                                     FRINMTAATVLAALSSS-----VFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAV
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 Length 635;
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/ Match 10.8%; Score 407.5; DB 2; Local Similarity 24.4%; Pred. No. 1.6e-20; nes 158; Conservative 111; Mismatches 258;
  Query Match
Best Local S:
Matches 158
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ferrichrome-iron receptor 1 - Synechocystis sp. (strain PCC 6803)

(Synechocystis sp. C. Specien s111409)

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(Synechocystis sp. C. Specien s111409)

(Synechocystis sp. C. Specien s111409)

(Synechocystis sp. C. Specien s111409)

(Colore: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000)

(Colore: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000)

(Colore: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000)

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RESULT 42
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31; 266 IRGFGNQFS----DTVPILRDGFRLYGGFQGITEVSHLQQVEVLKGPSSILYGQIEPGGV 321 :|| |:| INLNSKKPLNEPFAEVEVQLGNQGLVRPRFDISGGLNPSGNLRYRLNGVYSNEASFRDFN 381 ...--PAD 270 OPLERFAYAPIVTYAİTDÖTDÜSLAVEYINDTNPADFÖLSSFGDGVAPVPRSRVINDPSD 441 271 ANNKLPSLPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFA 330 IVNK-----NFISAGYN------LEHRFNENWKLRNAFRYMSYNYDYNV--- 479 331 GSKLGMKTPAGRPGCNT--ADDKACAVGLGTEIKQKALAFDASYSRPFRLGNTANEFVIG 388 ADYNRFRSTNEQGRTTLYARGGLALN----EFRSIPQVDLIANARKGVRGYSHTVATENL 444 DEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKT-LHKASKTKFTGYA----GAVY 498 577 -RLGIYLQDQVSLLENLILVAGLRYDTITQNTNNLQTDFNQGGNTQQTDSAVTPRIGLLY 635 RPIPEISFFSNYSQSFTPNSGIDISGNPLEPERGEGFEIGVKAELFEQOLLTTLTYFNIS 695 SNSRDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGITSSAGMH--------662 Gaps -AVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117 696 KNNVAVSDPVNPLPLST----IGTQQSQGIELDIVGEILPGWKIIGNYSYINAKVTEDTD 751 RINMTA-ATVLAA----LSSSVFAAQTADLETVHIKGQRSYNAIVT-EKNGDYSSF---- 58 -RGY--EYSEYNIDGLPAQMQSIN----GTLPNLFAFDRVEVMRGPSGLFDSSGEMGGI VNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVM-AQTVGASPRPAE DLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMK DKNAAA--PLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQI--KTA C;Keywords: iron transport F;240-375/Domain: tonB-dependent receptor amino-terminal homology <TN F;581-863/Domain: tonB-dependent receptor carboxyl-terminal homology 10.6%; Score 402; DB 2; Length 863; ilarity 22.2%; Pred. No. 6.38-20; Conservative 127; Mismatches 335; Indels 136; 663 --AGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPG KNNRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGL-----Similarity Matches 171; Query Match Best Local 322 6 59 208 170 229 382 442 480 389 445 199 969 559 615 752 118 803 셤 g g ઠે ò δ

C;Species: Yersinia enterocolitica C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 29-Sep-1999 C;Accession: 822673 #824 #86 # C;Accession: 822673 # A G; Hantke, K. Mol. Microbiol. 6, 1309-1321, 1992 MyTitle: Perrioxamine uptake in Yersinia enterocolitica: characterization of the recepto A;Reference number: 822673; MUID:92349959; PMID:1640832 ferrioxamine receptor precursor - Yersinia enterocolitica RESULT 43

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A;Molecule type: DNA
A;Residues: 1-710 <BAE>
A;Cross-references: EMBL:X60447
C;Genetics:
RESULT 44
C83588
probable hydroxamate-type
C;Species: Pseudomonas aer
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F;27-710/Product: ferrioxamine receptor #status predicted <MAT>
F;84-220/Domain: tonB-dependent receptor amino-terminal homology <TNN
F;433-710/Domain: tonB-dependent receptor carboxyl-terminal homology
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C;Superfamily: ferrichrome-in
C;Keywords: membrane protein
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                                                                                                                       DAMAAY---RFTPKLK---LQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KRPQFTSECHFRLTAGNNNTQVAAFDYTDAISEHWAFR----LTGITRNSDTMYDHQREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180;
                                                                                                      DASVRADLGTWAASLKGAFVQLNVNNIADKKYVAAC-YSTSYCYWGAERSVQATVGYDF
                                                                                                                                                                            NDGNTPVLAPSNMASLWAQYEA-----GYGINVGAGIRYIGKQWADDANTLRVPSYTLG
                                                                                                                                                                                                               RDDGIFLLMPKHSANLWTTYQVTPELTIGGGVNAMSGI-----TSSAGMHAGGYATF
                                                                                                                                                                                                                                                   DVANRAVP-----ATYYVPAGKVNSQGLELEARSQISDRLSVIAGYTYNRVKFKDAIDG
                                                                                                                                                                                                                                                                                      D-KNAAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNS
                                                                                                                                                                                                                                                                                                                          DSGISPYVSYSQAITPSLFPDAQQXLLKPMTSEQYEVGIIYQPPGSTSLYSAALYDLTQN
                                                                                                                                                                                                                                                                                                                                                            NDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVG--YKGSYMDDRLNARVSFYRMK
                                                                                                                                                                                                                                                                                                                                                                                               GVYLQDEM-TLDNWHLNLSGRYDRMKTENINNTANSTDERTDNHAS-----GRASLLYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                   GIYGKSTFHPADGLSLIGGGRLGHYKIE-----SGEGKTLHKASKTKFTGYAGAVYDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSDRTLMNRYYS----GEDSSLNAFAVDNQLEADLRTAAVKHKVLLGVDFQKFRNNLRSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDGE-----SNHNVFKRWQQIYSYEFSHKFDDVWSFRQ-NASYTHSNTQLEQVYQGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVY----ARGYE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAFIIKRSA--ILCSLAMFIPLASIAD-DTIEVTAKAGHEADL--PTSGYTATTTKGATK
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aeruginosa
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                  ferrisiderophore
                  receptor PA0470 [imported]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 C;Accession: C83588 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Fo.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A;Cross-references: GB:AE004484; GB:AE004091; NID:g9946320; PIDN:AAG03859.1; GSPDB:GN001
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VGGANTENIPGSERTWTANLRYSE
                                   ARYVGSTYGDQANTYDGYAGSYTLYDAAVRYDLGQLNGSLKGVSVAVNANNLFNKDYLAS
                                                                   VNAMSGI----TSSAGMHAGGYATFDAMAAY---RFTPKLK---LQINADNIFNRHYYAR
                                                                                                     DNLKMIGAYSYADTEVKKGQYAGNRLQQA-----
                                                                                                                                   PKWQIHAGYSYLHSQIKT---ASNSRDDGIFLLMPKHSANLWTTYQ----VTPELTIGGG
                                                                                                                                                                       VGS--DSLFTAAV--YDLRQENVSVSQNIGGTPVTSQT----
                                                                                                                                                                                                                                          SRDKKFSGNAALSYIFDNGVAPYISYAESFQPTTGADMNSTSSLKPTEGKQWEIGVKYQP
                                                                                                                                                                                                                                                                          ASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADG-KLLKPRQGNQFEVGYK---
                                                                                                                                                                                                                                                                                                              TLGGRE---DWVHTGAT----FYNK-----
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                                                                                                                                                                                                        -GSYMDDRLNARVSFYRMKDKNAAAPLN----PNNKKTRYAALGKRVMEGVETEISGAVT
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Pred. No. 1.4e-19;
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PRNOASLWADYTWHEGTLNGFSVGAG
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probable ferrichrome iron receptor precursor [imported] - Escherichia coli (strain O157: C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli C;Species: Bacherichia coli Bacherichia coli Bacherichia coli Bacherichia coli Bacherichia C;Accession: E9118 R;Hayasah; T.; Makino, K.; Mara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. Dia, Reference mumber: A; Solot A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: E9118 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-713 cHAY>
A;Cross-references: GB:BA000007; PIDN:BAB37340.1; PID:g13363390; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC53917
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----AQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAA 187
                                        | | | | : :|||||:|| : :
GSSYVQADSFNS---DMAIYDRVEVLRGAAGMMKGAGGTAGGVNFVRKRGQDTAHTQLSL 283
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Poole K., Neshat S., Krebes K., Heinrichs D.E.;
"Cloning and nucleotide sequence analysis of the ferripyoverdine
receptor gene fipvA of Pseudomonas aeruginosa.";
J. Bacteriol. 175:4597-4604(1993).
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Pseudomonas.
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01-FEB-1996 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
- TIN-2002 (Rel. 41, Last annotation update)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
       EMBL; AE004666; AAG05786.1; -.
PIR; A40601; A40601.
InterPro; IPR00531; TonB boxC.
Pfam; PF00593; TonB boxC.
PROSTITE; PS00410; TONB DEPENDENT REC_1; FALSE_NEG.
PROSTITE; PS01156; TONB DEPENDENT REC_2; 1.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASLREIPOSVSIITNOQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNI 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.8%; Score 821.5; DB 1; Length 815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
FERRIPYOVERDINE RECEPTOR.
TONB C-TERMINAL BOX.
Y -> F (IN REF. 1).
MISSING (IN REF. 1).
S -> R (IN REF. 1).
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EMBL; U07359; AAB60199.1; -.
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PROSITE; PSO1156; TONB DEPENDENT REC 2; 1.
PROSITE; PSO1156; TONB DEPENDENT REC 2; 1.
Outer membrane; Iron transport; Transport; TonB box;
SIGNAL 1
47
POTENTIAL.
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                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                 Bitter W., Marugg J.D., de Weger L.A., "The ferric-pseudobactin receptor PupA homology to TonB-dependent Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Ferric-pseudobactin 358 receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WCS358;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas putida
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                                                                    EMBL; X56605; CAA39942.1; -.

BIR; S15169; S15169.

InterPro; IPR000531; TonB_boxC.

Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                                                                                         . Microbiol. 5:647-655(1991) FUNCTION: SPECIFIC RECEPTOR PSEUDOBACTIN 358.
                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     [_TaxID=303;
                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                                          requires a license agreement (Son email to license@isb-sib.ch).
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FERRIC-PSEUDOBACTIN
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                                                                                                                               -PNNKKTRYAALGKRVMEGVET-----EISGAVTPKWQIHAGYSYLHSQIKTASNSRD
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; 1B36164F86207951 CRC64;
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Pred. No. 4.3e-45;
                                                                      LTIGGGVNAMSGITSSAGMH-----AGGYATFDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=KI2;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=8905232;
MEDLINE=97061202; PubMed=R., Haba T., Haba T., Alba H., Baba T., Etbl T., Kajihara M., Kanai K., Kaahimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Satto N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                       MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sauer M., Hantke K., Braun V.;
"Ferric-coprogen receptor FhuE of Escherichia coli: processing and agequence common to all TonB-dependent outer membrane receptor proteins.";
J. Bacteriol. 169:2044-2049(1987).
-!- FUNCTION: REQUIRED FOR THE UPTAKE OF IRON(III) VIA COPROGEN, FRRIOXAMINE B. AND RHODOTORULIC ACID.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SUBCELLULAR LOCATION: THE TONB AND THE EXBB PROTEIN HAVE TO
                                                                                                                                           Sauer U., Hantke K., Braun V.; "Sequence of the fhuE outer-membrane receptor gene of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                        K12 and properties of mutants."; Microbiol. 4:427-437(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87194585; PubMed=3032906;
                                                                                              STRAIN=K12;
MEDLINE=90286919; PubMed=2162465;
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STRAIN=K12 / MG1655;
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PIR; A26875; A26875
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V->P: ABOLISHES TRANSPORT ACTIVITY.
G->A-V, V, D, H: IMPAIRED TRANSPORT AND GROWTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 NDKEINKVFMTLKQQFADTWQATLNATHSEVEFDSKMMYVDAYVNKADGMLVGPYSNYGP
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                                                                                                                                                                                DB 1; Length 729;
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                                                                                                             G -> C (IN REF. 1).
68ACEE7D110F76CD CRC64;
                                                                                                                                                                                                     Best Local Similarity 27.3%; Pred. No. 4.2e-43; Matches 211; Conservative 148; Mismatches 308;
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fe(III)-pyochelin receptor precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U03161; AAC43213.1; -. EMBL; AE004839; AAG07609.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opportunistic pathogen.";
Nature 406:959-964(2000).
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STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437333; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=PAO / IA602;
MEDLINE=94117363; P
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STRAIN=PAO / IA602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane; Iron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phenolate siderophore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "FptA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: HIGH-AFFINITY OUTER MEMBRANE RECEPTOR REQUIRED TRANSPORT OF FE(III)-PYOCHELIN.
SUBCELLULAR LOCATION: Outer membrane.
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DRYRAEVDVGGPLSASGNVRGRAVA---AYEDRDYFYDVADQGTR--LLYGVTEFDLSPD
                                                                                             LIGNTASSPQDMAIYERVEILRGSNGLLHGTGNPAATVNLVRKRPQREFAASTTLSAGRW
                                                                                                                              IPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYNIDGLPA 132
                                              KQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRP----AEKNNRHETFYAAADWDINPD
                                                                                                                                                                                               LPQSASVIDHERLEQQNLFSLDEAMQQATGVTVQPFQLLTTAYYVRGFKVDSFELDGVPA
                                                                                                                                                                                                                                                                                                  LALSPLAAAVADARKDGETELPDMVISGE---STSATQPPG-----
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PS01156; TONB DEPENDENT REC 2; 1.
mbrane; Iron transport; Transport;
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Pred. No. 1.3
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DA796313116E0CC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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01-OCT-1994 (Rel.
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                           MEDLINE=93316856; PubMed=8392140;
Koster M., van de Vossenberg J., Leor
"Identification and characterization
                                                                                                                                                                                                                                                                                                                                                                    STRAIN=WCS358;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Ferric-pseudobactin BN7/BN8 receptor precurso
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                                                                                                     FUNCTION: SPECIFIC RECEPTOR FOR THE SIDEROPHORES FERRIC PSEUDOBACTIN BNB AND FERRIC PSEUDOBACTIN BN7, IRON CHELATING PSEUDOBACTIN BN7, IRON CHELATING PSEUDOBACTIN BN7, IRON CHELATING PSEUDOBACTIN BN7, IRON FROM THE ENVIRONMENT, SPECIALLY UNDER IRON-RESTRICTED CONDITIONS.
SUBCELLULAR LOCATION: Outer membrane.
SUBCELLULAR LOCATION: Outer membrane.
INDUCTION: BY IRON LIMITATION IN ADDITION TO THE PRESENCE OF OF THE TWO COGNATE PSEUDOBACTINS BNB OR BN7.
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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                                                                                                                     FERRIC-PSEUDOBACTIN BN7/BN8 RECEPTOR
                                                                                                                                                                                                                                                                                                              SSVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL
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                                                                                                                                                                                                Matches 197; Conservative 154; Mismatches 314; Indels 101;
                                                                                                                                                                           DB 1; Length 809;
                                         PIR; $32899; $32899.
InterPro; FRR000531; TonB boxC.
Pfam; PF00593; TonB boxC; 1.
PROSITE; PS00430; TONB DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; Signal; Receptor.
SIGNAL
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                                                                                                                                POLY-SER.
TONB C-TERMINAL BOX
                                                                                                                                                                           18.8%; Score 708.5; DB 1 25.7%; Pred. No. 4.8e-41;
           send an email to license@isb-sib.ch)
                                                                                                                                                      809 AA; 88389 MW;
                               EMBL; X73598; CAA51995.1;
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PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor;
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Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
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IDBNITPICATION BY MASS SPECTROMETRY, AND PUTATIVE FUNCTION.
IDBNITPICATION BY MASS SPECTROMETRY, AND PUTATIVE FUNCTION.
MEDLINE=20267815; PubMed=10806384;
Molloy M.P., Herbert B.R., Slade M.B., Rabilloud T., Nouwens A.S.,
Williams K.L., Gooley A.A.;
"Proteomic analysis of the Escherichia coli outer membrane.";
"Proteomic analysis of the Escherichia coli outer membrane.";
Eur. J. Blochem. 267:2871-2881 (2000).
-:- FUNCTION: PROBABLE RECEPTOR, TONB-DEPENDENT, THAT PARTICIPATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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--- SUBCELLULAR LOCATION: Outer membrane (Potential).
--- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mau B., Shao Y.; "The complete genome sequence of Bscherichia coli K-12.";
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                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable tonB-dependent receptor ybiL precursor.
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MEDLINE=97061202; Pubmed=8905232;
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Pfam; PF00593; TonB_boxC; 1.
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15-DEC-1998
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SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spietl
                                                                                                                                                                                Q56145;
01-NOV-1997
                                                                                                              Salmonella typhimurium
                                                                                                                         FOXA OR STM036
                                                                                                                                                     15-JUN-2002
15-JUN-2002
                                                                                 Salmonella
                                                                                                                                                                                                             FOXA
                                                                   NCBI_TaxID=602;
                                                                                              Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                  YI-----GSMHKGSDGAVGTPAFTEGYWVADAKLGYRVNRNLDFQLNVYNLFDTDYVAS
                                                                                                                                                                                                                                                                                                                                                                                         NITPAWQVIGGYTQQKATIKNGKDVAQDGSSSLPYTPEHAFTLWSQYQATDDISVGAGAR
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                                                                                                                                                  (Rel. 35, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                              subdivision;
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-!- FUNCTION: FERRIOXAMINE BINDING AND UPTAKE, IN
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EMBL; U62282; AAB04552.1; -.
HSSP; P06971; 1BY5.
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
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Tsolis R.M., Baumler A.J., Stojiljkovic I., Heffron F., Fur regulon of Salmonella typhimurium: identification
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Kingsley R.A., Reissbrodt R., Rabsch W., Ketle
Everest P., Dougan G., Baeumler A.J., Roberts
"Ferrioxamine-mediated iron(III) utilization b
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{\tt RGFSDGSLDNVYLDGLKMMGDTNSHSSLVVDPWFLEDIEVVRGPASVLYGRSSPGGIVAL
                        RGYEYSEYN---IDGLP--AQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNL
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Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FERRIOXAMINE BINDING AND UPTAKE, IN ASSOCIATION WITH THE
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"Ferrioxamine uptake in Yersinia enterocolitica: characterization the receptor protein FoxA.";
Mol. Microbiol. 6:1309-1321(1992).
                                                      RYALMPSLTWRITDRTRLDLMAYPHRDPEGGSHSGLPYQGT-VVPYNG------GKI
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SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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MEDLINE=92349959; PubMed=1640832;
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PROSITE; PSO1156; TONB\_DEPENDENT\_REC\_2; 1.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport; Length 710; Indels 82EB6EC1546900B8 CRC64; POTENTIAL. FERRIOXAMINE RECEPTOR ilarity 23.3%; Pred. No. 5e-20; Conservative 127; Mismatches 334; DB 1; C-TERMINAL the European Bioinformatics Institute. There were by non-profit institutions as long a modified and this statement is not removed entities requires a license agreement (See h Score 401.5; POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. or send an email to license@isb-sib.ch) POTENTIAL. POTENTIAL. POTENTIAL POTENTIAL POTENTIAL POTENTIAL TONB HSSP; P06971; 1QJQ. InterPro; IPR000531; TonB\_boxC. Pfam; PF00593; TonB\_boxC; 1. 78382 MW; 10.6%; EMBL; X60447; CAA42975.1; -. 3317 344443 317 317 317 317 317 317 317 317 618 632 657 679 Transport, TonB box.
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01-APR-1988 (Rel. 07, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update
Ferrichrome-iron receptor precursor (Ferric
                                             SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
MEDLINE-94261430; PubMed-8202364;
FUJITA N., MOTI H., Yura T., Ishihama A.;
"Systematic sequencing of the Escherichia coli
the 2.4-4.1 min (110,917-193,643 bp) region.";
 STRAIN-K12
                                                                                                                                           Coulton J.W., Mason P., Cameron D.R., C
"Protein fusions of beta-galactosidase
receptor of Escherichia coli K-12.";
J. Bacteriol. 165:181-192(1986).
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"Crystal structure of the antibiotic albomycin in complex with outer membrane transporter FhuA.";

Protein Sci. 9:956-963 (2000).

-I- FUNCTION: THIS RECEPTOR BINDS THE FERRICHROME-IRON LIGAND.

INTERACTS WITH THE TONB PROTEIN, WHICH IS RESPONSIBLE FOR E COUPLING OF THE FERRICHROME-PROMOTED IRON TRANSPORT SYSTEM.

AS A RECEPTOR FOR BACCTERIOPHAGE T5 AS WELL AS T1, PHI80 AND COLICIN M. BINDING OF T5 TRIGGERS THE OPENING OF A HIGH CONDUCTANCE ION CHANNEL. CAN ALSO TRANSPORT THE ANTIBIOTIC
                                                                                                                                                                                                                               Ferguson
Welte W.;
                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS)
MEDLINE=20306978; PubMed=10850805;
Ferguson A.D., Braun V., Fiedler H.-P.
                                                                                                                                                                                                                                                                                                                   "Transmembrane signaling across the ligand-gated crystal structures of free and ferrichrome-bound allosteric changes.";
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Davis K., Federspiel N., Hyman R., I
Lashkari D., Lew H., Lin D., Namath
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE=99074366; PubMed=9856937;
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Mol. Gen. Genet. 209:49-55(1987).
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MEDLINE=99081293; PubMed=9865695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Energy-coupled transport through the outer membrane of Escherichicoli small deletions in the gating loop convert the FhuA transport protein into a diffusion channel.";
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Pfam, PF00593; TonB boxC.

PROSITE; PS00430; TONB DEPENDENT REC 1; 1.

PROSITE; PS01156; TONB DEPENDENT REC 2; 1.

Outer membrane; Iron transport; Transport; TonB box; Sign
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PIR; S45219; S45219.
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PR0SITE; PS001156; TONB_DEPENDENT_REC_2; FALSE_NEG.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
Signal; Receptox; Transmembrane; Outer membrane; Iron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sauvage C., Franza T., Expert D., "Analysis of the Erwinia chrysanthemi ferrichrysobactin receptor gene: resemblance to the Escherichia coli fepA-fes bidirectional
                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                        EMBL; X87967; CAA61205.1; -. HSSP; P06971; 2FCP.
                                                                                                                                                                                                                                                                                   modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             This
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-i- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE CHRYSOBACTIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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STRAIN=1223-75-1, 8081, YE737, and 1209-79;
RAKIN A., Heesemann J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR THE BACTERIOCIN PESTICIN AND FOR THE SIDENOPHORE YERSINIABACTIN.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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01-NOV-1995 (Rel. 32, Last sequence update)
06-CCT-2010 (Rel. 40, Last annotation update)
Pesticin receptor precursor (IRPC) (IPR65).
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STRAIN=ATCC 51871 / WA-314 / Sero
MEDLINE=95075311; PubMed=7984105;
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                                                                                                                                 transport;
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1C20E0352FAD4DCC CRC64;
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EMBL; Z35104; CAA84487.1; -.

EMBL; U09530; AAA69906.1; -.

EMBL; AU031866; CAA21395.1; -.

EMBL; AJ414150; CAC90722.1; -.

HSSP; P05825; 1FEP.

InterPro; IPR000531; TonB boxC.

Pfam; PF00593; TonB boxC; 1.

PROSITE; PS00430; TONB DEPENDENT REC_1; PALSE_NEG.

PROSITE; PS00430; TONB DEPENDENT_REC_2; FALSE_NEG.

Signal; Receptor; Transmembrane; Outer membrane; Iror

Transport; TonB box; Complete provence.
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"Analysis of the pesticin receptor from Yersinia iron-deficient growth and possible regulation by J. Bacteriol: 177:1824-1833(1995).
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Bacteria; Proteobacteria;
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AC P173T5;
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                                                         SEQUENCE FROM N.A. MEDIAGE 2644220; MEDIATRE=8123100; PubMed=2644220; MADLIATE=8123100; J.; Monisky J.; Monisky J.; Monisky J.; Monisky J.; Expolutionary relationship between the TonB-dependent outer membrane transport proteins: nucleotide and amino acid sequences of the Escherichia coli colicin I receptor gene."; J. Bacteriol. 171:1041-1047(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-59 FROM N.A., AND SEQUENCE OF 26-46.
MEDLINE=88058737; PubMed=3316180;
Griggs D.W., Tharp B.B., Konisky J.;
"Cloning and promoter identification of the iron-regulated cir gene of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIDSALZ / MG165,
STRAIDSALZ / MG165,
BHBULINB=9742617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=K12 / BHB2600;
Richterich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90264362; PubMed-2160948; Griggs D.W., Kafka K., Nau C.D., Konisky J.; Activation of expression of the Escherichia coli cir gene by an iron independent regulatory mechanism involving cyclic AMP-cyclic
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMP receptor protein complex.";

4. Bacteriol. 172:13529-3533(1990).

-!- FUNCTION: NOT YET KNOWN. POSTULATED TO PARTICIPATE IN IRON TRANSPORT. OUTER MEMBRANE RECEPTOR FOR COLICINS IA AND IB.

-!- SUBSCELLULAR LOCATION: Outer membrane.

-!- INDUCTION: BY IRON AND BY A CYCLIC AMP/CYCLIC AMP RECEPTOR PROTEIN COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                           Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steffes C., Ellis J., Wu J., Rosen B.P.; "The lysP gene encodes the lysine-specific permease."; J. Bacteriol. 174:3242-3249(1992).
                                                                                                                                                                                 REVISIONS.
Nau C.D., Konisky J.;
J. Bacteriol. 171:4530-4530(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 169:5343-5352(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92250419; PubMed=1315732;
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EMBL, U00007; AAA66531.1; -.
EMBL, AE000304; AAC75216.1; -.
EMBL, M19225; AAA23581.1; -.
EMBL, M89774; AAA17054.1; -.
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                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                            Church G.M.;
                 Escherichia
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EcoGene; EC10155; cirA.
InterPro; IPR00531; TonB boxC.
Pfam; PF00593; TonB boxC; I.
PROSTTE; PS00430; TONB DEPENDENT REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 VGADWN-KFKM---NSHDVFADLKHYFGNGGYGKVGMRYSDRDADS------NYA-- 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSRDGNVEFAWTPNQNHDFTA-----GY---GFDRQDRDSDSLDKNRLERQNYSVS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------FAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRP 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 HNGRWDYGTSELKYYGEKVENKNP------GNSSPITSESNTVDGKYTLP 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 FRLGNTANEFV-IGADY-----NRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLI 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 L---TAINOFLTVGGEWRHDKLSDAVNLTGGTSSKTSASQYAL--FVEDEWRIFEPLALT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            426 ANARKGVRGYSHTVATENLDEFGIYGKS-----TFHPADGLSLIGGGRLGHYKIESGE 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNOFEVG--YKGS-----YMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYA 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMPKHSAN-----LWTTYQVTPELTIGGGVNAMSGITSSAGMHAGGYATFDAMA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            479 GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKL-----LKPRQ 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 WATAPKAP---------SLLQLSPDWTSNSCRGACKIVGSPDLKPET 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 267; DB 1; Length 663;
ilarity 20.6%; Pred. No. 7.9e-11;
Conservative 108; Mismatches 237; Indels 240; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAE
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TONB BOX.
TONB C-TERMINAL BOX.
S -> D (IN REF. 6).
I -> N (IN REF. 1).
W, 2C68A45D4B5EE414 CRC64;
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PIR; S24561; S24561.
HSSP; P05825; 1FEP.
ECO2DBASE; B068.1; 6TH EDITION.
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73895 MW;
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663 AA;
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SIGNAL
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. Smith K.A., Spencer D.H., Wong G.K.R., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSEAE
                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M98033; AAA25928.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restricted the supplementary of the supplementary of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    opportunistic pathogen.";
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STRAIN=ATCC 15692 /
MEDLINE=20437337; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dean C.R., Poole K.;
"Cloning and characterization of the ferming energinosa.";
gene (pfeA) of Beseudomonas aeruginosa.";
J. Bacteriol. 175:317-324(1993).
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HSSP; P05825; 1FEP.
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                                                                                                                                                                                                                                                                                                                      InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TÖNB_DEPENDENT_REC_1; PALSE_NEG
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Coller membrane; Iron transport; Transport; TonB_boxer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93123148; PubMed=8419284
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
INDUCTION: BY IRON AND ENTEROBACTIN. SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR
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                                                                                                                                                                                                 POTENTIAL.

FERRIC ENTEROBACTIN R
TONB BOX.

TONB C-TERMINAL BOX.
                                                                                                  Score 256.5; DB 1
Pred. No. 4.9e-10;
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                                                                        Mismatches 321;
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                                                                                                                                                                                                                                                                                                                        box;
                                                                           Indels 209;
                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                        Signal;
                                                                                                                         746;
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Yuan Y.,
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    SEQUENCE FROM N.A.
STRAIN=Rd / KW20 /
MEDLINE=95350630; P
Fleischmann R.D., A
                                                                                                                                                   15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                         NCBI_TaxID=727;
[1]
                                                                                                                           Hypothetical HI1466.1.
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                                                                                                                                                                                                                        HAEIN
                                                                                                 Bacteria;
                                                                                                            Haemophilus influenzae
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                                                                                                                                                                                                                                                                           DKRLF-RAGNAQGVVGIDGAGAATYNEPG--RTFYTSLTASF
                                                                                                                                                                                                                                                                                                                               SLQATVTWYGKQKPKKYDYHGDRVTGSANDQLSPYAIAGLGGTYRLSKNLSLGAGVDNLF
                                                                                                                                                                                                                                                                                                                                                                                                               ISGAVT-----PKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLNSDGSVRGRVMAQTVG--ASPRPAEKNN-RHETFYAAADWDINPDTVL--GAGYLYQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                           YSHDGLVAGLTYFRNDYKNKIESGLSPVDHASGGKGDYANAAIYQWENVPKAVVEGLE--
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                                                                                                 Proteobacteria;
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                                                                                                                                        tonB-dependent
                                                                                                                                                                                                         STANDARD;
/ ATCC 51907;
PubMed=7542800;
Adams M.D., White O.,
                                                                                                                                                41, Created)
41, Last sequence update)
41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                         ---SGITSSAGMHAGGYATFDAMAAYRFTPKLKLQINADNIF
                                                                                                                                                                                                                                                                                                     -GANTFNI PGSERTWTANLRYSF
                                                                                                 gamma
                                                                                                                                        nnotation update)
                                                                                                 subdivision; Pasteurellaceae;
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                                                                                                                                                                                                          345
     Clayton
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     Kirkness
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     E.F.,
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anguillarum (Listonella anguillarum)
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                   Plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                   "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 YSHTVATE-------KLDEFGIYGKSTFHPADGLSLIGGGRLGHY-----K 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474 IESG-----EGKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTN--LDADGKL 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7 LKPRQCNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGV 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETEISGAVTPKWQIHAGYSYLHSQIKTASNSRD-----DGIFLLMPKHSANLWTTYQ 638
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Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soctt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finc L.D., Fritchman J.L., Ruhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                     white O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J., Halckey B., Dodson R., Gwinn M., Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 345;
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Pfam; PF00593; TonB_boxC; 1.

PROSITE; PS01156; TÖNB_DEPENDENT_REC_2; FALSE_NEG.

Hypothetical protein; Receptor; TonB_box; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Conservative 58; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 AA; 38744 MW; BAF83C55FCC9CB2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     687 ADNIFNRHYY-ARVGGANTFNIP---GSERTWTANLRYSF 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.9%; Score 221.5; DB 1
24.1%; Pred. No. 4.2e-08;
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AC P11461; P19830;
DT 01-0CT-1989 (Rel. 12, Created)
DT 01-0CT-1989 (Rel. 12, Last sequence update)
DT 16-0CT-2001 (Rel. 40, Last annotation update)
DF 16-DF PATA.

GN FATA.
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                                                                                                                                             Science 269:496-512(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Listonella
                                                                                                                                                                                                                                                                                                                                                            66 IPASLREIPQSVSIITNQQVKDRNV-DTFDQLARKTPGLRVLSNDDG--RSSVYARGY-- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKRPTKA----VSGSLNSDGSVRGR 214
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                                                                                                                                                                       Actis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.; "Genetic and molecular characterization of essential components c
the Vibrio anguillarum plasmid-mediated iron-transport system."; J. Biol. Chem. 263:2853-2860(1988).
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Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS004310; TONB_DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 215.5; DB 1; Length 726; 21.6%; Pred. No. 3.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TONB C-TERMINAL BOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                       MEDLINE=88139336; PubMed=2830268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; TonB box; Plasmid.
                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 637-726 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J03529; AAA91581.1; -.
EMBL; M34504; AAA79859.1; -.
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726
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726
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PIR; PQ0051; PQ0051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    726 AA;
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                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=El Tor N16961 / Serotype O1;

STRAIN=El Tor N16961 / Serotype O1;

STRAIN=El Tor N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dedson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.

McDonald L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.(
SEQUENCE OF 1-151 FROM N.A.
STRAIN-Classical Ogawa 395 / ATCC 39541 /
MEDLINE=91072235; PubMed=2174861;
Goldberg M.B., Boyko S.A., Calderwood S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P27772; Q9KUPO;
01-AUG-1992 (Rel. 23, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Classical Ogawa 395 / ATCC 39541 / MEDLINE=93023868; PubMed=1406279; Goldberg M.B., Boyko S.A., Butterton J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Payne S.M., Calderwood S.B.; "Characterization of a Vibrio cholerae virulence factor homologous the family of TonB-dependent proteins."; Mol. Microbiol. 6:2407-2418(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iron-regulated outer membrane virulence
IRGA OR VC0475.
                                                                                                                                                                                                    "DNA sequence of both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYDLNDNNSLYLSLSQLYTPQTNLDAD----GKLLKPRQGNQFEVGYKGSYMDDRLNARV
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, Sellers P.,
, White O.,
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Best Local Similarity
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J. Bacteriol. 172:6863-6870(1990).
-I- FUNCTION: INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING FERRIC VIBRIOBACTIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Receptor; Complete proteome. SIGNAL 1 25 POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Virulence; Outer membrane; Iron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U72152; AAC44766.1; -. EMBL; AE004134; AAF93648.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
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TIGR; VC0475; -.
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PIR; S25265; S25265.
337
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SUBCELLULAR LOCATION: OULEY membrane.
MISCELLANEOUS: REGULATION OF THE IRGA EXPRESSION IS NEGATIVE
REGULATED AT THE TRANSCRIPTIONAL LEVEL BY IRON.
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
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                                                                                                                                                                                                                                                                    NLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVS
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                            GTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFR
                                                                                    HYFGNGGYGKVGMRYSDRDADS-----NYAFAGSKLGMKTPAGRPGCNTADDKACAVGL
                                                                                                                   VSAQDRENNVGKSAQSSGCRGTCSNTDNQYRR--NHVAVSHQGDW-----
                                                                                                                                                                             ANFFVTGPLSDALSLQVYGQTTQRDEDEIEHGYGDKSLRSLTSKLNYQLNPDHQLQLEAG
                                                                                                                                                                                                           GSLNSDGSVRGRVMAQTVGASPRPAEKNNRH-----ETFYAAADWDINPD--TVLGAG
                                                                                                                                                                                                                                        PLOAIERIEVIRGPMSTLYGSDAIGGVINIITRKDQQQWSGNVQLSTVVQENRASGDEQS
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19.6%;
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TONB C-TERMINAL |

D -> G (IN REF.

K -> Q (IN REF.

A -> T (IN REF.
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Pred. No. 3.4e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A95F82FEC072EC93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 305;
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Q (IN REF. 1).
T (IN REF. 1).
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                                                                 524
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SIPOVDLIANARKGVRGYSHTVATENLDEFGIYGKSTFHP-----ADGLSLIGGGRLG 470
                       374 LAEQFRLTFGGR------LDHDKNYG-SHFSPRVYGVWNLDPLWTVKGG--- 415
                                                                                                    KLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN-----PNN----KKTRYA 576
                                                                                                                       -----LTAFHNDFKDKITRVACPANICTAGPNQWGAAPTYRV 507
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                                                                                                                                                                                                                                  566 WOTTDRINSWANLNYRGKEMOPEGGASNDDFIAPSYTFIDTGVTYALTDTATIKAAVYNL 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Riley M., Collado-Vides J., Glasner H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE TONB-DEPENDENT RECEPTOR YNCD.
TONB C-TERMINAL BOX.
7B3B96C6ABA48FE4 CRC64;
                                                  HYKIESG-EGKTLHKASKT--KFTGYAGAVY---DLNDNNSLYLSLSQLYTPQTNLDADG
                                                                                                                                                                       577 ALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLMPKHSANLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     box;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EcoGene; EG13774; yncD.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PR051TE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
Hypothetical protein; Outer membrane; Receptor; Signal; TonB l
                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable tonB-dependent receptor yncD precursor.
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                                                      Gapa
                                                                                                    5 MSVFRINMTAATVLAALSSSVPAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGT 64
                                                                                                                                                     -------DEQTMIVSAAP 35
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vitamin B12 receptor precursor.
BTUB OR STM4130.
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Ouery Match 5.7%; Score 214; DB 1; Length 700; Best Local Similarity 20.0%; Pred. No. 3.8e-07; Matches 156; Conservative 114; Mismatches 317; Indels 192;
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InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Conserved struct typhimurium btuB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=LT2 / SGSC1412 / A1CC / MEDLINE=21534948; PubMed=11677609;
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Wei B.Y., Bradbeer C., Kadner R.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Salmonella enterica serovar Typhimurium
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SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: COBALAMIN RECEPTOR PROTEIN. ALSO ACTS AS BACTERIOPHAGE BF23 AND IS NECESSARY FOR THE UPTAKE
                           RHETFYAAAD-----WDINPDTVLGAGYLYQQRHLAPYN-GLPADANNKLPSLPQHVFV
                                                                                                                                   NIDGLPAQMQSINGTLPNLFAF-----DRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA
                                                                                                                                                                RSAVLAPVTIVTRODIERWOSTSVNDVLRRLPGVDIAQSGGAGQNSSIFIRGTNSSHVLV
                                                                                                                                                                              QS-----VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG--RSSVYARGYEYSB--Y 125
                                                                                                                                                                                                                     ATLLTAFSVTAFSAWAQD------TSPDTLV-----
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 LSKTLYGALEHTFSDRWS---GFVRGYGYDNRTDYDAYYSPGSPLIDTRKLYS--
                                                      TELTAGWGSNSYQNYDISTQQQLGENTRATLIGDYEYTKGFDVVAKGGTGMQAQPDRDGF
                                                                                FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGR---
                                                                                                           LIDGVRLNLAGVSGS-ADLSQFPVSLVQRIEYIRGPRSAIYGSDAIGGVVNIITTRDNPG
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PS01156; TONB_DEPENDENT_REC_2; 1.
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No. 1.3e-06;
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                        "Novel two-component transmembrane transcription control: of iron dicitrate transport in Escherichia coli K-12."; J. Bacteriol. 172:6749-6758(1990).
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16-OCT-2001 (Rel.
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                                                                                                              Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; ucleic Acids Res. 23:2105-2119(1995).
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B., Staudenmaier H., Bra
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Pfam; PF00593; TonB_boxC, 1.
PROSTIE; PS001430; TONB_DEPENDENT_REC_1; 1.
PROSTIE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLPA------QMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Outer membrane.
-!- INDUCTION: FOR INDUCTION THE TONB AND THE EXBB PROTEIN HAVE TO ACTIVE. REGULATION BY THE IRON LEVEL MEDIATED BY THE FUR PROTEIN AND INDUCTION BY CITRATE PLUS IRON SUGGEST THAT THE IRON(III) DICITRATE COMPLEX MUST ENTER THE PERIPLASM WHERE IT BINDS TO A TRANSMEMBRANE PROTEIN, WHICH REGULATES DIRECTLY OR VIA A FURTHER INDUCTOR, TRANSCRIPTION OF THE FEC GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 108; Mismatches 316; Indels 250; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 LAGLSFSAFAAQVNIAPGSLDKALNQYAAHSGFTLSVDASLTRGKQS-NGL----HGDYD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SSFAVTV----GTKIPASLREIPQSVS 78
                                                                                   transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRON(III) DICITRATE TRANSPORT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYARGYEYSEYN-----ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:| | || || || GIPVPFAPYGQPQLSLAPVSLGNM---DAIDVVRGGGAVRYGPQSVGGVVNFV---TRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----TADLETVHIKGQRSYNAIVTEKNGDY-
                                     Staudenmaier H., van Hove B., Yaraghi Z., Braun V.;
"Nucleotide sequences of the fecBCDE genes and locations of the proteins suggest a periplasmic-binding-protein-dependent transpormechanism for iron(III) dicitrate in Escherichia coli.";
mechanism for 171:2626-2633 (1989).
-!- FUNCTION: FECA IS THE OUTER MEMBRANE RECEPTOR PROTEIN IN THE IRON(III) DICTIRATE TRANSPORT SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T -> A (IN REF. 1).
A -> T (IN REF. 1).
T -> M (IN REF. 1 AND 3).
W -> R (IN REF. 1).
L -> V (IN REF. 1).
L -> V (IN REF. 1).
K -> A (IN REF. 1).
W; 16BSBS10276C3B09 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 205; DB 1;
Pred. No. 1.8e-06;
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TONB
                        MEDLINE=89213950; PubMed=2651410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000499; AAC77247.1; -. EMBL; M63115; AAA23768.1; -. EMBL; M26397; AAA23761.1; -.
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EcoGene; EG10286; fecA.
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774
16
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774 AA;
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Matches 170; Conserv
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Stojiljkovic I.;
Submitted (SPP-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS PROTEIN IS INVOLVED IN THE INITIAL SIEP OF IRON
UPTAKE BY BINDING HEMIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS
THE BACTERIA TO EXTRACT IRON FROM THE ENVIRONMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                  319 SDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRL 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPSAHEVGVGYRYLN-ESTHEMRYYTATSSGQLPSG---SSP---YDRDTRSGTEAHAW- 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               439 VATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGK----TLHKASKTKFTGYA 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604
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ONNPKETHNLMV 283
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SEQUENCE FROM N.A.

STRAIN=ARCC 51872 / WA-C / Serotype O:8;

MEDLINE=93049186; Pubmed=1425573;

Stojiljkovic I., Hantke K.; Furshinia enterocolitica: similarities with Hamin uptake system of Yershinia enterocolitica: similarities with other TonB-dependent eyetems in Gram-negative bacteria.";

EMBO J. 11:4359-4367(1992).
                                                                                 284 GGTADNGFGTALLYSGTRGSDWREHSATRIDDLMLKSKYAPDEVHTFNSLLQYYDGEADM
                                                                                                                                                                                                                                                    PA-----DANNKLPSLPQHVFVGADWNKFKMNS--HDVFADLKHYFGNGGYGKVGMRY
                                                                                                                                                                                                                                                                                                                            344 PGGLSRADYDADRWQSTRPYDRF----WGRRKLASLGYQFQPDSQHKFNIQGFYTQTLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SGYLEOGKRITL------SGYLEOGKRITL-------SGYLEOGKRIEPRYSOIFMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 NVLYHLTDSWNLYANTEGSFGTVQYSQIGKAVQSGNVEPEKARTWELGTR--YDDGALTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEGVETEIS---GAVTP---KWQIHAGY
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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Best Local :
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SIGNAL
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pir; S28042; S28042.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane; Iron transport; Transport; TonB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPREAEKNNRHETFYAAADWDINEDTVLGAGYLYQQRHLAEYNGLEADANNKLESLEQHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y--NIDGLPAQMQS--INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV-----NL 172
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 ASYF --- DTNA--
                               VSFYRMKDKNAAAPLNPNNKKTRYAALGKRVMEG-------VETEISGAVTPKW
                                                                                                      VYDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMD-----DRLNAR
                                                                                                                                                                                                            FPQADI-RFGSGWLQDEITL------RDLP-VSILAGTRYDNYRGSSEGYADVDA 420
                                                                                                                                                                                                                                             VIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR-KGVRGYSHTVATENL 444
                                                                                                                                                                                                                                                                                                                      -TPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNT-----ANEF 385
                                                                                                                                                                                                                                                                                                                                                                                          FVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMK-----
                                                                                                                                                                                                                                                                                                                                                                                                                              N---APNDETISNVLAKGTWRIDQIQSLSANLRY----YNNSALEPKNPQTSAASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLPGQNSGYRVYSAAATGDHSFGLGASAFGRTDDVDGILSFGTRDIGNIR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLTLVDGIRQGTDTGHLNSTFLDPALVKRVBIVRGPSALLYGSGALGGVISYETVDAADL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGR----SSVYARGYEYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRWSPLSLAIACTLSLAVQAADTSSTQT-NSKKRIADTMVVTATGNERSSF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIP 67
                                                                                                                                         DKWSSRGAVSVTPTDWLMLFG---------SYAQAFRAPTMGE
                                                                                                                                                                          DEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKTKFTGYA-----GA
                                                                                                                                                                                                                                                                                  ARPQGTP----EEGRKQTTKGGKLENRTRLFTDSFASHLLTYGTEAYKQEQTPSGATES
                                                                                                                                                                                                                                                                                                                                                           NLMTDRSTIQRDAQ-----
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PS00136; TONB DEPENDENT REC_2; FALSE NEG.
PS01156; TONB DEPENDENT REC_2; FALSE NEG.
Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EAPMMVTVVEADTPTSETATSATDMLRNIPGLTVTGS--GRVNGQDVTLRGYGKQG 112
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687 AA;
                                                                  NDSKHFSMNIMGNTLTNYWVPNPNLKPETNETQEYGFGLRFNDLMMAEDDLQFK
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687 H
51 T
687 T
75226 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.3%;
-KDYISTGVTMDFGFGPGGLYCKNCSTYSTNIDRAKIWGW
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TONB C-TERMINAL BOX.
; 69092EF97F5DC08A CRC64;
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Pred. No. 3.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
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                                                                                                           Query Match
Best Local Similarity
Matches 174; Conserv
                                                                                                                                                                                                                   SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                           Receptor.
SIGNAL
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: RECEPTOR FOR CLOACIN DF13/AEROBACTIN.
-i- SUBCELLULAR LOCATION: Outer membrane.
-i- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Krone W.J.A., Stegehuis F., Koningstein G., van Doorn C., Roosendaal B., de Graaf F.K., Oudega B.; "Characterization of the pColV-K30 encoded cloacin DF13/aerobactin outer membrane receptor protein of Escherichia coli; isolation and purification of the protein and analysis of its nucleotide sequence and primary structure."; FEMS Microbiol. Lett. 26:153-161(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IUTA EC
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EMBL; X05874; CAA29298.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1990 (Rel.
01-NOV-1995 (Rel.
15-JUL-1999 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000531; TonB_boxC
Pfam; PF00593; TonB_boxC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S01042; S01042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS.
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                                                        SVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTK 65
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TLWALNPLILTMMAPA-----VAQQTDDETFVVSANRSNRTVA-----
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                                                                                                                                                                                                                                                                                                                                                                              PS00430; TONB_DEPENDENT_REC_1; 1.
PS01156; TONB_DEPENDENT_REC_2; 1.
mbrane; Iron transport; Transport;
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                                                                                                                                    Score 198;
Pred. No. !
                                                                                                                                                                                                                                         FERRIC AEROBACTIN RECEPTOR TONB BOX.
TONB C-TERMINAL BOX.
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  (See http://www.isb-sib.ch/announce/
                                                                                                                                 5e-06;
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                                                                                                                                                             DB 1; Length 732;
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                                                                                               193
                                                                                                                                                    -----QYKAEADV--SGSINSDGSVRGRVMAQTVGASPRPAEKNNRHETFYAAA 240
                                                                                                                                                                                                           --- DWDINPDTVLGAGYLYQQRHLAPY--NGLPADANNKLPSLPQHVFVGADWNKFKMNS 295
                                                                                                                                                                                                                                                                                                                                                 PTVNA-------NKQVTAFSSSQQDTDQYGMKLTLNSKPMDGWQITWGLDADH 372
                                                                                                                                                                                                                                                                                                                                                                                                        ERFTS-NOMFFDLAQASASGGLNNKKIYTTGRYPSYDITNLAAFLOSGYDINNLFTLNGG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANLWITYQVTPELTIGGGVNAMS-----GITSSAGMHAGGYATFDAMAAYRFTPKL 681
                                                                  100 VVL-VDGVRLNSSRTDSRQLDSIDP----FNMHHIEVIFGATSLY-GGGSTGGLINIVT 152
                                                                                                                          153 KKGQPETMMEFEAGTKSGFSSKDHDERIAGAVSGGNEHISGRLSVAYQKFGGWFDGNGD 212
                                        SEYNIDGL------PAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLVR 174
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                                                                                                                                                                                                                           PGCNTADDKACAVGLGTEIKQKALAFDAS-----YSRPFRLGNTANE-----FVIGADY
                                                                                                                                                                                                                                                                                                                                                                              392 NRFRSTNEQ--GRTTLYARGGL-----ALNEFRSIPQVDLIANARKG------VRGY
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                                                                                                                                                                                                                                                                  296 HDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGR----
                                                                                                                                                                                 213 ATLLDNTQTGLQYSDRLDIMGTGTLNIDESRQLQLITQ------
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                KR----PTKAFQGHAAAGFGTHK--------
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STRAIN-KIM6;
MEDLINE-96386041; PubMed-9026634;
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HMUR OR YPO0283.
Yersinia pestis.
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EMBL; AJ414141; CAC89146.1; -..
InterPro; IPR000531; TOAB boxC.
Pfan; PF00593; TOAB boxC; 1...
PROSITE; PS00410; TOMB DEPENDENT REC\_1; 1..
PROSITE; PS01156; TOMB\_DEPENDENT\_REC\_2; FALSE\_NEC.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor; MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebainia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,
"Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).

-I- FUNCTION: THIS PROTEIN IS INVOLVED IN THE INITIAL STEP OF IRON UPTAKE BY BINDING HEMIN, AN IRON CHELATIN SIDEROPHORE THAT ALLOWS THE BACTERIA TO EXTRACT THOON FROM THE ENVIRONMENT.

-I- SUBCELLULAR LOCATION: Outer membrane.

-I- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS. SVSIITNOOVKDRNVDTFDQLARKTPGLRVLSNDDGRSS---VYARGYBYSEY--NIDGL 130 MYTVIEGNAPTSQTAATAADMLRQVPGLTVTGS--GRTNGQDVVMRGYGKQGVLTLVDGV 120 131 PAQMQS--INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV-----NLVRKRPTKA 180 181 FQGHAAAGFGTH-----KQYKAEADVSGSLN----SDGSVRGRVMAQTVGASPRPAEKN 230 231 NRHETFYAAADWDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQHVFVGADWNK 290 ETISNVLAKGTWQIDSIQSLSANLRY-----YNNSAIEPKNPQTSAPSSTNVMTNRST 285 FKWNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMK-----TPAGRPG 344 214; Gaps LAALSSSVFAAQTADLETVHIKGQR--SYNAIVTEKNGDYSSFAVTVGTKIPASLREIPQ 75 LAIACTLPLATQAADTTTTQTSSKKHSTDTMVVTATGNERSSF------EAPM 62 YRVYSSAATGDHSFGLGASAFGRTDDLDGILSFGTRDIGNIR----QSNGFN---APND οţ Hornung J.M., Jones H.A., Perry R.D.; "The hmu locus of Yersinia pestis is essential for utilization free haemin and haem-protein complexes as iron sources."; Mol. Microbiol. 20:725-739(1996). Length 676; Query Match
5.2%; Score 195; DB 1; Length 67
Best Local Similarity 19.1%; Pred. No. 7.2e-06;
Matches 147; Conservative 104; Mismatches 306; Indels 84ED731CB914ACD3 CRC64; HEMIN RECEPTOR.
TONB BOX.
TONB C-TERMINAL BOX. send an email to license@isb-sib.ch). Biovar Orientalis; 74230 MW; 28 676 51 676 659 ( 676 AA; SEQUENCE SIGNAL 16 18 92 63 181 291 or RRARE REPORTED TO THE REPORT OF THE REPORT O 유 d g ò ò 엄 6 ò ò 셤 ò 임

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Blattner F.R., Plunkett G TTT TELLINE
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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MEDLINE=97061202; PubMed=8905232; Oshima T., Aiba H., Baba T., Fuji Ikemoto K., Inada T., Itoh T., Ka
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Chung E., Allen E., Araujo R., Aparicio A., Davis Federspiel N., Hyman R., Kalman S., Komp C., Kurdi Lin D., Namath A., Oefner P., Roberts D., Schramm Submitted (JAN-1997) to the EMBL/GenBank/DDBJ data
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"Nucleotide sequence of the gene for the "T-thrishia coli. Homology among
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EMBL; AE000163; AAC73685.1; --
EMBL; U82598; AAB40783.1; ALT_INIT.
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EMBL; J04216; AAA23756.1; --
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J. Biol. Chem. 263:18857-18863(1988).
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PROSITE;
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Escherichia coli.";
Biol. 6:56-63(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchanan S.K., Smith B.S., Venkatramani L., Xia D., Esser I
Palnitkar M., Chakraborty R., van der Helm D., Deisenhofer
"Crystal structure of the outer membrane active transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                        PROSITE; PS00430; TŌNB_DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Transmembrane; Outer membrane; Iron transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90354449; PubMed=2201687; Armstrong S.K., Francis C.L., McIntosh
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J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99101384; PubMed=9886293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCT. Biol. 6:56-63 (1999).

PUNCTION: THIS PROTEIN IS INVOLVED IN THE INITIAL STEP OF IRC PUNCTION: THIS PROTEIN IS INVOLVED IN THE INITIAL STEP OF IRC UPTAKE BY BINDING FERRIENTEROBACTIN (FE-ENT), AN IRON CHELATI SIDEROPHORE THAT ALLOWS E.COLI TO EXTRACT IRON FROM THE ENVIRONMENT. FEDA ALSO ACTS AS A RECEPTOR FOR COLLICINS B AND SUBCELLULAR IOCATION: Integral membrane protein. Outer membra SUBCELLULAR IOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                       PF00593;
                                                                                                                                                            Receptor; 3D-structure; Complete
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chem. 265:14536-14543(1990).
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Pred. No. 1.1e
8; Mismatches
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                 Score 193.5; DB 1;
Pred. No. 1.1e-05;
                                                           A -> R (IN REF. 1).
MISSING (IN REF. 1).
; 09348AAB1C29710A CRC64;
                                                                                                                                  FERRIENTEROBACTIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o K., Masuda S.,
a Y., Nashimoto H
, Takemoto K., Wa
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C-TERMINAL BOX.
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Wada C., Yan
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o Y., Saito
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VSIITNQQVKDRNV-DTFDQLARKTPGLRVLSN-----DDGRSSVYARGYEYSEYNID

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                                              GLPAQMQS------INGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIVNLV 173
                                                                                                               174 RKRPTKAFQGHAAAGFGT--HKQ----YKAEADVSGSLNSDGSVRGRVMAQTVGASPRPA 227
                                                                                                                                                                                EKNNRHETFYAAAD-----WDINPDTVLGAGYLYQQRHLAPYNGLPADANNKLPSLPQH 281
                                                                                                                                                                                                                                                  VFVGAD-----WNKFKMNSHDVFADLKHYFGNGGYGKVGMRYS-DRDADSNYAFAGSKL 334
                                                                                                                                                                                                                                                                                                                 ----PAGRPGCNTA--DDKACAVG 356
                                                                                                                                                                                                                                                                                                                                                GDETNRLYRONYALTWNGGWDNGVTTSNWVQYEHTRNSRIPEGLAGGTEGKFNEKATQDF 359
                                                                                                                                                                                                                                                                                                                                                                                 LGTEIKQKALAFDASYSRPFRLGNTANEFVIGADYNRFR----STNEQGRTTLYARGGLA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QTNLDADGKLLKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLNPNNK 571
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30-WAY-2000 (Rel. 39, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Rhizobactin receptor precursor (TonB-dependent siderophore receptor
                                                                  | : : | | | | | | | | TKKGSGEWHGSWDAYFNAPEHKEEGATKRTNFSLTGPLGDEFSFR-------
                                                                                                                                                                                                               -----LYGNLDKTQADAWDIN-------QGHQSARAGTYA---TTLPAGREG
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Rhizobium meliloti (Sinorhizobium meliloti)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.lab-sib.ch/announce/
or send an email to license@isb-sib.ch).
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PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
Outer membrane; Iron transport; Transport; TonB box; Signal; Receptor; Plasmid; Complete proceeme.
                                                                                             biosynthesis,
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268 KQDSDYGLYYGPFFAALADPSLFETRSGYESDFNPQTRRSMLNVTYTDNDVFGQQLLLQG 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GTKIPASLREIPQSVSIITNQQVKDRNVDTFD------QLARKTPGLRVLS 107
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Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells I.
Yeh K.-C., Davis R.W., Federapiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymk megaplasmid.",
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
-: FUNCTION: RECEPTOR FOR THE SIDEROPHORE RHIZOBACTIN.
-: SUBCELLULAR LOCALION: OUTER TONB-DEPENDENT RECEPTOR PROTEINS.
STRAIN=RCR2011 / SU47;
MEDLINE-21172875; PubMed-11274118;
Lynch D., O'Brien J., Welch T., Clarke P., Cuiv P.O., Crosa J.H.
O'Connell M.;
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larity 18.9%; Pred. No. 1.1e-05;
Conservative 116; Mismatches 308; Indels 277;
                                                                                         "Genetic organization of the region encoding regulation, bio and transport of rhizobactin 1021, a siderophore produced by Sinorhizobium melloti."

J. Bacteriol. 183:2576-2585(2001).
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729 746 TONB C-TERMINAL BOX.
746 AA; 80633 MW; 16AE44A4025D5B23 CRC64;
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RHIZOBACTIN RECEPTOR
                                                                                                                                                                                                                                 MEDLINE=21396509; PubMed=11481432;
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EMBL; AE007312; AAK65923.1; -.
InterPro; IPR00531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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Best Local Similarity
Matches 163; Conserv
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SEQUENCE FROM N.A.
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RESULT 27
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P06129;
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MEDLINE=94089392; PubMed=8265357;
Blattner F.R., Burland V.D., Plun
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01-OCT-1993 (Rel. 27, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Vitamin B12 receptor precursor.
BTUB OR BFE OR CER OR DCRC OR B3966.
  Gustafsson C., Lindstroem P.H., Bjoerk G.R.; The trmA promoter has regulato
                                                                      SEQUENCE OF 1-5 FI
MEDLINE=91154132;
                                                                                                                                             "Analysis of the Escherichia coli genome. region from 89.2 to 92.8 minutes."; Nucleic Acids Res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=85130824; PubMed=3882670; Heller K., Kadner R.J.;
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regulatory
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EMBL; U00006; AAC43072.1; -.
EMBL; A5000471; AAC76948.1; -.
EMBL; M57568; -; NOT ANNOTATED CDS.
EMBL; L14556; AAA23676.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Point mutations in a conserved region (TonB box) of Escherichia outer membrane protein BtuB affect vitamin B12 transport.";
J. Bacteriol. 171:6526-6533(1989).
-i- FUNCTION: COBALAMIN RECEPTOR PROTEIN. ALSO ACTS AS A RECEPTOR BACTERIOPHAGE BF23 AND IS NECESSARY FOR THE UPTAKE OF E COLIC
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Dougherty T.J., Thanassi J.A., Pucci M.J.;
"The Escherichia coli mutant requiring D-glutamic
of mutations in two distinct genetic loci.";
J. Bacteriol. 175:111-116(1993).
                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                 EcoGene; EG10126; btuB.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
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PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Cobalt transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                           PIR; A21892; QRECET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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MEDLINE=90078094; Pubmed=2687240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed proin the genome of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       common with the rRNA P1 promoter family of Escherichia coli.", J. Bacteriol. 173:1757-1764(1991).

    -!- SUBCELLULAR LOCATION: Outer membrane.
    -!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kadner R.J.
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MEDLINE=97443975; PubMed=9298646;
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RSTVLAPTTVVTRQDIDRWQSTSVNDVLRRLPGVDITQNGGSGQLSSIFIRGTNASHVLV
                          QS-----VSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDG--RSSVYARGYEYSE--Y 125
                                                     ASLLTACSVTAFSAWAQD
                                                                              ATVLAALSSSVFAAQTADLETVHIKGQRSYNAIVTEKNGDYSSFAVTVGTKIPASLREIP
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19.7%;
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V->G: INACTIVATE UPTAKE.
A -> G (IN REF. 1).
A -> R (IN REF. 1).
A -> R (IN REF. 1).
                                                                                                                         Score 191;
Pred. No. 1
                                                                                                                                                                                                                       TONB C-TERMINAL BOX.
L->P: INACTIVATE UPTAKE
                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                VITAMIN B12 RECEPTOR
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                                                     -TSPDTLV-
                                                                                                          Mismatches
                                                                                                                                                                                                                                                   BOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
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                                                                                                                         DB 1;
.2e-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        612 KTASNSRDDGIFLLMPKHSANL---WTTYQVTPELT---IGGGVNAMSGITSSAGMHAGG 665
NIDGLPAQMQSINGTLPNLFAF----DRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKA 180
                        |||: ::|::|::||
LIDGVRLNLAGVSGS-ADLSQFPIALVQRVEYIRGPRSAVYGSDAIGGVVNIITTRDEPG 157
                                                                                                                                                                                                                                                           --OSWD-----28HSKDYNY---- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DARNAITDTPLIRRAKOQVKYQLDWQLYDFDWGITYQYLGTRYDKDYSSYPYQTVKMGG 563
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-!- FUNCTION: RECEPTOR FOR THE HYDROXAMATE SIDEROPHORE, FERRICHROME.
BINDS ALSO TO MOST OTHER FERRICHROME DERIVATIVES EXCEPT ENANTIO
FERRICHROME AND FERRIC HODOTOWILATE.
-!- SUBCELLULAR LOCATION: OUTER membrane.
-!- INDUCTION: BY IRON STARVATION. IRON REGULATION MEDIATED THROUGH
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STRAIN=Serotype O:8;
MEDLINE=93311281; PubMed=8384682;
Koebnik R., Hantke K., Braun V.;
"The TonB-dependent ferrichtrome receptor FcuA of Yersinia enterocolitica: evidence against a strict co-evolution of receptor structure and substrate specificity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S64 VSLWDLAVAYPVTSHLTVRGKIANLFDKDYBTVYG----YQTAGREYTLSGS--YTF 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             666 YATFDAMAAYRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLRYSF 722
                                                                                                                                                 N---RHETFYAAAD---WDINPDTVLGAGYLYQQRHLAPYN-GLPADANNKLPSLPQHVF
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                                                                                                                                                                                                                                                                                                                                  ------DPHYGRYDSSATL----DEMKQYTVQW-------ANNVIVGHGS
                                                                                                                                                                                                                                                                                                                                                                                                         331 IGAGVDWQKQTTTPGTGYVEDGYDQRNTGIYLTGLQQVGDFT------F
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                                                                                                             TEISAGWGSNSYONY----DVSTQQQLGDKTRVTLLGDYAHTHGYDVVAYGNTGTQAQTD
                                                                                                                                                                                    NDGFLSKTLYGALEHNFTDAWSGFVRGYGYDNRTNYDAYYSPGSPLLDTRKLYS----
                                                                                                                                                                                                                      VGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYS------DRDADSNYAFAG
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(Rel. 32, Last sequence update)
(Rel. 33, Last annotation update)
                                                                          FQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVMAQ-
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01-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 DGRSSVYARG----YEYSEYNIDGLPAQMQSINGTLPNLFA----FDRVEVMRGP---- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 ASVQNVRGYGNPSQNYRIRGYNLDGDDISFGGLFGVLPRQIVSTSMVERVEVFKGANAFI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAGFGTHKQYKAEADVSGSLNSDGSVRGRVM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQTVGASPRPAEKNNRHETFYAAADWDINPD---TVLGAGYLYQQRHLAPYNGLPADANN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIPEPPSSTLNYGQSW------VYTDMETTF-----GMLRSEYDVSQNWTVYGS 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KLGMKTPAGRPGC----NTAD-----DKACAVG-----LGTEIKQKALA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 VGASRNEETGOYGAPMLTNNNGDATISRLYVPYVADSVAGLGGIRGHFDTGPITHKVNLG 417
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                                                                                                                                                                                                                                                              PROSITE; PS00430; TÖNB DEPENDENT REC 1; 1.
PROSITE; PS01156; TONB DEPENDENT REC 2; 1.
Signal; Receptor; Transmembrane; Outer membrane; Iron transport;
                   SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.0%; Score 190.5; DB 1; Length 758; 19.8%; Pred. No. 1.7e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                   81749 MW; 945675B0DEF49F7C CRC64;
                                                                                                                                                                                                                                                                                                                                                             FERRICHROME RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                            TONB BOX.
TONB C-TERMINAL BOX
                                                                                                                                                                                                         EMBL; X67331; CAA47746.1; -.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
                                                                                                                                                                                                                                                                                                                     Transport; TonB box. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                   758 AA;
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Best Local :
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01-OCT-1993
01-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M96731; AAA25503.1; -. PIR; A43335; A43335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cornelissen C.N., Biswas G.D., Tsai J., Paruchus Thompson S.A., Sparling P.F.; "Gonococcal transferrin-binding protein 1 is recutilization and is homologous to TonB-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria gonorrhoeae.
Bacteria; Proteobacteria; beta subdivision;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00593; TonB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=92394880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferrin-binding protein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors."
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- FUNCTION: ACTS AS A TRANSFERRIN RECEPTOR AND IS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSFERRIN UTILIZATION.
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-RGYEYSEYN--IDGLPAQMQS---
                                                                                    FAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGLRVLSNDDGRSSVYA 117
                                                                                                                                 QQQHLFRLNILCLSLMTALPAYAENVQAGQAQEKQLDTIQVKAKKQKTRRDNEVTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane;
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PS01156; TONB_DEPENDENT_REC_2; 1.
mbrane; Receptor; Signal; TonB box
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(Rel. 32, Last annotation updat
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                                          LGKLVKTADTLSKEQVLD----IRDLTRYDPGIAVVEQGRGASSGYS
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Pred. No. 0
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01-FEB-1995
16-OCT-2001
SEQUENCE OF 25-45
STRAIN=CCUG 37603
MEDLINE=93307625;
                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE STRAIN=CCUG 37603 / B1686 / Serco MEDLINE=93345825; PubMed=8344530;
                                                                                                                                                                      Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision;
NCBI_TaxID=491;
                                                                  encoding
                                                                                                                                                                                                                 TBP1
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                                                      3ene 130:73-80(1993).
                                                                                                                                                                                                                           Transferrin-binding protein
                                                                             'Cloning
                                                                                          Jacobs E.,
                                                                                                     egrain M., Mazarin V.,
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                                                                                                                                                                                                                                                                                                                                                              EMYGWRSGDKIKAVKIDPEKSFNK
                                                                 and characterization of
the transferrin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -YDRQGIGLDNHFQ---QTHCSAD---GSDKYCRPSADKPFSYYKSDRVIYGES---
                                                                                           Schryvers A.B.;
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                             STANDARD;
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 / B16B6 / Serogroup
PubMed=8319886;
                                                                                                                               AND SEQUENCE OF 25-42.
B16B6 / Serogroup B /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HKLLQAAFKKSFDTAKIRHNLSVNLGYDRFGSNLRHQD
                                                                                                      Irwin S.W.,
                                                                                                                                                                                                                             1 precursor
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Tbp1 and Tbp2.
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Griffiths E., Stevenson P., Byfield P., Ala'Aldeen D.A.,
Borriello S.P., Holland J., Parsons T., Williams P.;
"Antigenic relationships of transferrin-binding proteins from
Neisseria meningitidis, N. gonorrhoeae and Haemophilus influenzae:
Eross-reactivity of antibodies to NH2-terminal peptides.";
PEMS Microbiol. Lett. 109:85-91(1993).
-!- FUNCTION: ACTS AS A TRANSFERRIN RECEPTOR AND IS REQUIRED FOR
TRANSFERRIN UTILIZATION.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SUBCELLULAR LOCATION: Outer membrane.
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFERRIN-BINDING PROTEIN 1.
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908 TONB C-TERMINAL BOX.
101583 MW; FE2FF4974CAC3C31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4%; Score 167.5; DB 1
18.2%; Pred. No. 0.00085;
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Pfam; PF00593; TonB boxC; 1.
PR051TE; PS00430; TONB DEPENDENT REC 1; 1.
PR051TE; PS01156; TONB DEPENDENT REC 2; 1.
Outer membrane; Receptor; Signal; TonB box.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.2%;
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PIR; S33154; S33154.
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908 AA;
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RLGNTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANAR----KGV 432
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-i- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
-i- SIMILARITY: LOW, TO THE CORRESPONDING PROTEIN IN SEROTYPE D
HINPLUENZAE.
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Haemophilus.
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STRAIN=D142 / Serotype B;
STRAIN=D142 / Serotype B;
MEDLINE=95270579; PubMed=751272;
Cope L.D., Yogev R., Mueller-Eberhard U., Hansen B.J.;
"A gene cluster involved in the utilization of both free hemepexin by Haemophilus influenzae type b.";
J. Bacteriol. 177:2644-2653(1995).
-I- FUNCTION: REQUIRED FOR UTILIZATION OF FREE HEME AT I
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InterPro; IPR000531; TonB boxC.
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RESULT 32
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PROSITE; PS01156
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                                                                                                                                                                                                                                                                                         TANLHFDSLF---KQGDKFKIEATYFRNDVKDFINLKIFNDAKTNTNASASAGAGAGANP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPNALDLLKNNDKFGVKIROGYQTANNLSERDVSVFAANDKFDVLISGFYNNADNL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVYARGYEYSEYNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLFDSSGEMGGIV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATSVAAALEDIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSVFRINMTAATVLAALSSSVFAAQTADLETVHIKGQR--SYNAIVTEKNGDYSSFAVTV 62
                                                                                                                                                                   SNIAASKIGVGVNYALVKDKFTVGATVTHYAAQRRVPKDHSVTYPSYILTDLRATY--AP
                                                                                                                                                                                                L-MPKHSANLWTTYQ-VTPELTIGGGVN---AMSGITSSAGMHAGGYATFDAMAAYRFTP
                                                                                                                                                                                                                                                                                                                       --NLDADGKLLKPRQGNQF--EVGYKGSYMDDRLNARVSFYRMKDKNAAAP-----LNP
                                                                                                                                                                                                                                                                                                                                                     IVTNWLDFTAKYNEAFRAPSMQERFVSGSHFGTSILGRNEINKFVANPNLRPETAKNKEI
                                                                                                                                                                                                                                                                                                                                                                                                              TTGVYLIAHIPLFGEK-----LLLSPSVRYDHYDTSS---KTVKYKDNHLSPATKLTW
                                                                                                                                                                                                                                                                                                                                                                                                                                             TVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTL----HKASKTK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SELSHISFVYGVDYMRDKIRTERGTNNKDA-----QFRADPY-----NAN----SN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AN----EFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STVFNYYLTPDNPYLNTHIALYNNKTIEKEQRKVS-GVKDQTKLT----TRGINLRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAFDASYSRPFRLGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -EVENELTNEQITDQIREFHKPNNGSPPKAKPSQEEFYSGVKTRFGSVSY-LTDQQIPDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADANNKLPS-----LPOHVFVGADWNKFKVNSHDVFADLKHYFGNGGYGKVGMRYSDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAQTVGASPRPAEKNNRHETFY-----AAADWDINPDTVLGAGYLYQQ-RHLAPYNGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNFDLAHRGSYF----LPMSL-----IQEIEVIKGPSSSLWGSGALGGVVAMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTKIPASLREIPQSVSIITNQQVKDRNVDT---FDQLARKTPGLRVLSND------DGRS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRFSKLSLAIATTLVTANA---LAQSVELDSINVIATRDPSRFAYTPEKQSK-DSLLSKQ
                                                                                                                                     -----KLKLQINADNIFNRHYYARVGGANTFNI-PGSERTWTANLRYSF
                                                                                                                                                                                                                               NGALLPTKSQYQNITNARLSGIELQ-AQYQTERLTLFTNYG-----STKGKDKDSGEAL
                                                                                                                                                                                                                                                           NN----KKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFL
                                                                                                                                                                                                                                                                                                                                                                                  -----NLVR----KRPTKAFQGHAAAGFGTHKQY------KAEADVSGSLNSDGSVRGRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----RTGKGNKLNNTAYKQFGGLAKFGWQINDANRVELSHRETRFKQTAPSNN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PS01156; TONB_DEPENDENT_REC_2; 1.

mbrane; Transport; TonB box; Signal; Receptor.

0R 21 (POTENTIAL).

20 725 HEME/HEMOPEXIN_UTILIZATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 725 HEME/HEMOPEXIN UTII 725 AA; 80838 MW; FC7886E020CB5BCE
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                                 STANDARD;
   40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%; Score 165.5; DB 1; 20.1%; Pred. No. 0.00085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NVDIRGGSRSIAQK-PNIRGLSDNRVVQVIDGVR 101
    Created)
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Best Local Sim:
Matches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 404:502-506 (2000).
-!- FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OR HEMOGLOBIN/HAPTOGLOBIN COMPLEX AND IS REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T. Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., H. Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Ratherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G., Whitehead S., Spratt B.G., Barrell B.G., "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemoglobin-haptoglobin utilization protein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00430; TŌNB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Transport; TonB box; Signal; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL162753; CAB83769.1; -.
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MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=65699;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
SUBCELLULAR LOCATION: Outer membrane (Potential).
SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS:
                          SLPQHVFVGADWNKFKWNSHDVF-----ADLKHYFGNGGYGKVGMRYSDR---
                                                                                  GPSKYLTYVATGVARSQPDPQEW-VNKSTLFKLGYNFNDQNRIGWIFEDSRTDRFTNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSNDDGRSSVYA-RGYEYSE--YNIDGLPAQ-----MQSINGTLPNLFA-----
                                                                                                                                   KNNRHETFYAAA-----DWDINPDTVLGAGYLYQQRHLAPY---NGLPADANNKLP
                                                                                                                                                                                              ITAAGRLFGLDALLVYTRRFGKETKNRSTEGDI - - EIKNDGYV-
                                                                                                                                                                                                                                                        HAAAG----
                                                                                                                                                                                                                                                                                                          NFSEVTITKGADSLKSGSGALGGAVNYQTKSASDYVSEDKPYHLGIKGGSVGKNSQKFSS 196
                                                                                                                                                                                                                                                                                                                                                                                                                          VEGGRAGSNGFTIRGVDKDRVAINVDGL-AQAESRSSEAFQELFGAYGNFNANRNTSEPE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FPAFAADPAPQSAQTLNEITVTGTHKTQKLGEEKIRRKTLDKLLVNDEHDLVRYDPGISV
                                                                                                                                                                                                                                                                                                                                                                  - FDRVEVMRGPSGLFDSSGEMGGIVNLVRK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90570
                                                                                                                                                                                                                                 FGTH-KQYKAEADVSGSLNSDGSVRGRVMAQTVGASPRPAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TONB C-TERMINAL BOX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 293;
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                                                                                                                                                                                                                                                                                                                                                                  RPTKAFQG
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                                                                                                                                                                                                                                                                                                                                                                                       610
                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | : | : | : | : | : | 667 GK-ATQNNGKETPINALSP-----WTAV-----YSLGYDAPSKRWGINAYATRTAAKKP 714
                                      DADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKOKALAFD----ASYSRPF 376
                                                                          DIPKNYDKRGINGEVYHSFRHIRONTAQ-----WTADFEKQLDFSKAVWAAQYGLGG 414
                                                                                                                                                                                          519 NLDADGKLLKPRQGNQFEVGYKGS---------YM----DDRLNARV 552
                                                                                                                                                                                                                                                                                                                                                                                                                              553 SFYRMKDKNA--AAPLNPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAG--YSYLH 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQIKTASNSRDDGIFLLMPKHSANLWTTYQVTPELTIG-----GGVNAMSGITSSA-- 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------GMHAGGYATFDAMAAYRFTPKLKLQINADNIFNRHYYA----- 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.-J.,
NLWTGTTTSAATGDYR-HRQDVSYRRRSGVEYKNELEHGPWDSLKLRYDKQRIDMNTWTW 362
                                                                                                                                                                                                                                                                                                           494 AIRGQIPHLGSERAHAGFSYGTGFDWRFTKHLHL-LAKYSTGFRAPTSDETWLLFPHPDF 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, beta subdivision, Neisseriaceae, Neisseria
                                                                                                                  RLGNTANEFVIGADYNRFRSTNEOGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYS
                                                                                                                                                                                                                                                                     -- EGKTLHKASKTKFTGYA-GAVYDLNDNNSLYLSLSQLYT-------PQT
                                                                                                                                                                                                                                                                                                                                                                                       553 YLKANPN-LKAEKAKNWELGLAGSGKAGNFKLSGFKTKYRDFIELTYMGVSSDDKNNPR-
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-!- FUNCTION: ACTS A. TRANSFERRIN RECEPTOR AND IS REQUIRED FOR TRANSFERRIN UTILIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Outer membrane.
-!- INDUCTION: BY IRON STARVATION.
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=CCUG 37608 / M982 / Serogroup B / Serotype 9;
MEDLINE=93345825; PubMed=8344530;
                                                                                                                                                      GKGDNAN----SDYSYF-----AKLYDPKILASNQAKI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                       LFDSSGEMGGIVNLVRKRPTKAFQGHAAAG-FGTHKQYKAEADVSGSLNSDGSVRGRVMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 QTVGASPR------218 QTVGASPR------
                                                                                                                                                                                                                                               Query Match 4.3%; Score 161; DB 1; Length 911; Best Local Similarity 18.3%; Pred. No. 0.0024; Matches 178; Conservative 133; Mismatches 346; Indels 314;
                                                                                                                                                                TRANSFERRIN-BINDING PROTEIN 1.
                                                                                                                                                                               45 TONB BOX.
911 TONB C-TERMINAL BOX.
101631 MW; 99283ABAE0B773E6
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          EMBL, Z15130; CAA78833.1; -.
PIR; JN0821; JN0821.
PIR; S33156; S33156.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00193; TonB_boxC, 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Receptor; Signal; TonB_box.
SIGNAL
CHAIN
25 911 TRANSFERRIN-BIND
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   Outer membrane; I
SIGNAL 1
CHAIN 22
SITE 706
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STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Mguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P44600;
01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                        IDENTIFICATION BY MASS SPECTROMETRY.

MEDLINB-20137488; PubMed=10675023;

Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,

Gray C., Fountoulakis M.;

"Two-dimensional map of the proteome of Haemophilus influenzae."

Electrophoresis 21:411-429(2000).

Electrophoresis 21:411-429(2000).

-i- FUNCTION: PROBABLE RECEPTOR, TONB-DEPENDENT.

-i- SUBCELLULAR LOCATION: Outer membrane (Potential).

-i- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
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PROSITE; PS00430; TONB DEPENDENT REC 1; FALSE NEG.
PROSITE; PS01156; TONB DEPENDENT REC 2; 1.
Outer membrane; Receptor; Signal; TonB box; Complete |
SIGNAL 1 21 POTENTIAL.
CHAIN 22 723 PROBABLE TONB-DEPENDENT |
SITE 706 723 TONB C-TERMINAL BOX.
                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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Science 269:496-512(1995).
                                                                                                                                        EMBL; U32712; AAC21927.1; TIGR; HI0262; -.
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                                                                                                        InterPro; IPR000531;
Pfam; PF00593; TonB_
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                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
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                                                                                                                    IPR000531; TonB_boxC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria;
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(Rel. 32, Last sequence up
(Rel. 41, Last annotation
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(See http://www.isb-sib.
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                                                                                                                  MEGTGRNAKISAVYSF
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                                                                                                                                                                                                                                                                                                                        NPNNKKTRYAALGKRVMEGVETEISGAVTPKWQIHAGYSYLHSQIKTASNSRDDGIFLLM
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                                                                                                                                                                                                                                                                                                                                                                               -NLDADGKLLKPROGNOF--EVGYKGSYMDDRLNARVSFYRMKDKNAAAPL
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19.9%; Pred. No. 0.00
tive 114; Mismatches
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No. 0.0026;
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422 SDYSYF--
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=135720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 YSSFAVTVGTKIPASLREI----PQSVSIITNQQVKDRNVDTF-----DQLARKTPGLRV 105
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                                                                                                                                                                                                                                                                                                                                                                                             utilization operon of Neisseria meningitidis.";
Mol. Microbiol. 23:737-749(1997).
-!- FUNCTION: ACTS AS RECEPTOR FOR HEMOGLOBIN OR THE
HEMOGLOBIN/HAPPIGLOBIN COMPLEX MENDIS REQUIRED FOR HEME UPTAKE.
-!- SUBCELLULAR LOCATION: Outer membrane (Potential).
-!- SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                                                                                                                                                                                                                           STRAIN=DNM2 / Serogroup C / Serotype 2a;
MEDLINE=97206152; PubMed=9157245;
Lewis L.A., Gray E., Wang Y.-P., Roe B.A., Dyer D.W.;
"Molecular characterization of hpuAB, the haemoglobin-haptoglobin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 NKFKMNSHDVF-----DDDKHYFGNGGYGKVGMRYSDR-----DDDSNYAFAGSK
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HEMOGLOBIN-HAPTOGLOBIN UTILIZATION
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                           Hemoglobin-haptoglobin utilization protein B precursor.
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EMBL; U73112; AAC44893.2; -.
InterPro; IPR000531; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
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Conservative 109; Mismatches 315;
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-----PKI-LTSNQAK-----ITMLIENRSKYK 454
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                                                                                                         GKTLHKASKTKFTGYAGAVYDL---NDNNSLYLSLSQL
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                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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Pfam; PF00593; TonB_boxC; 1.
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MEDLINE=95350630; PubMed=7542800;
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PS01156; TONB_DEPENDENT_REC_2; 1.
PS01156; TONB_DEPENDENT_REC_2; 1.
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                                                                                                                           130 R--RVTVDKGNYSPQYGNGGFAGTVKFETKDARDFLQENQKIGGFLKYGNNSNNNQKTYS 187
                                                                                                                                                        197 AEADVSG-SLNSD----GSVRGRVMAQTVGASPRP-----AEKNNRHETFYAAADWDIN 245
                                                                                                                                                                              188 TALVLQNEQKVIDLLLFGSVR-----NAGDYKRPDNSKILFSKNNQ-KTGLIXLNWQIS 240
                                                                                                                                                                                                                                                                                                                                      ------ADYN-----RFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANA 428
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                                                                DQLARKTPGLRVLSN-DDGRSSVYARGYEYSE---YNIDGLPAQMQSI-NGTL---PNLF 145
                                                                                                             AFDRVEVMRGPSGLFDSSGEMGGIVNLVRKRPTKAFQGHAAAG----FGTH-----KQYK 196
                                                                                                                                                                                                    PDTVLGAGYLY-------OORHLAPYNGLPADANNKLPSLPQHVFVGAD--WNKFKM 293
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 Gaps
                                          ONSSNSNREELLPIIVNTNDD-----SNKLPGR-----SVLKQKNIEQXQADNA 69
                      ORSYNA-----IVTEKNGDYSSFAVTVGTKIPASLREIPOSVSIITNOOVKDRNVDTF 93
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                                                                                                                                                                                                                   --GVR-YDHINNIGQKNL-----HDYS
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Bacteria, Proteobacteria, delta subdivision, Myxobacteria,
Myxococcales, Cystobacterineae, Myxococcaceae, Myxococcus.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                            "Oar, a 115-kilodalton membrane protein required for development of
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                                  Farez-Vidal E., Inouye
                                                                                                                                                    J. Bacteriol. 175:4756-4763(1993).
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-!- SIMILARITY: LOCAL, TO TONB-DEPENDENT RECEPTOR PROTEINS.
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W; EA8C077296352EF0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
MEDLINE=93328680; PubMed=8335633;
Martinez-Canamero M., Munoz-Dorado J.,
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Matches 187; Conserv
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                                                                                                          VIUA VIBCH (
Q00964; Q9JQ00;
01-APR-1993 (Re)
                                                                                                                                                                                                                                                                                                           STRAIN-Classical Ogawa 395 / ATCC 39541 / Serotype O1;
MEDLINE=92276356; PubMed=1317381;
Butterton J.R., Stoebner J.A., Payne S.M., Calderwood S.B.;
"Cloning, sequencing, and transcriptional regulation of viuk,
gene encoding the ferric vibriobactin receptor of Vibrio chol
                                                                                                                                                                                                                                       STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype O1; Liao W.J., Choi M.H., Butterton J.R.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25,
01-APR-1993 (Rel. 25,
16-OCT-2001 (Rel. 40,
             This SWISS-PROT entry is copyright.
                                                                        Nature 406:477-483 (2000)
                                                                                  cholerae.";
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibriobactin receptor VIUA OR VC2211.
                                                                                             "DNA sequence of both chromosomes
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                                                                                                                                                                                                                                                                                                    Bacteriol.
                                  SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: LOCAL TO OTHER TONB-DEPENDENT RECEPTOR PROTEINS.
                                                            FUNCTION: RECEPTOR FOR FERRIC VIBRIOBACTIN.
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It is produced through a collaboration informatics and the EMBL outstation
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Best Local :
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00430;
Signal; Receptor;
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                           GKLLKPRQGNQF -- EVGYKGSYMDDRLNA
                                                                                 GGRLGHYKIESGE--GKTLHKASKTKFTGYAGAVYDLNDNNSLYLSLSQLYTPQTNLDAD
                                                                                                                                    GGLALNEFRSIPQVDLIANARKGVRGYSHTVATENLDEFGIYGK--
                                                                                                                                                               TYGIKAAKGYNASGAGLAFNSMOFTGFRPYEFEQESIWNYEFYTRHRFSHSVEVLT----
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127; Conserv
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687 F
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QGFEFSSNAAYTGSYFSESGNS
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TonB_box; Outer membrane; Transport;
                                                                                                                                                                                                                                                                           -----TLIGARY--YOSSODDMYIDAASAYPMDGRTKAKSVF--
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76413 MW;
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Pred. No. 0
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                                                                                                          SGDVFIANLDEASTYGAEIGSRWYATSSLELF-
                            550
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us-09-889-267-2.rsp

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395 RSTNEQGRTTLYARGGLALNEFRSIPQVDLIANARKGVRGYSHTV-ATENL------D 445
 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPEATED 31 TIMES.
-!- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN=168 / BGSC1A1;

MEDLINE=97124196; PubMed=8969509;

MODINE=97124196; PubMed=8969509;

Miwa Y., Fujita Y.;

Miwa Y., Fujita Y.;

Sequencing of a 65 kb region of the Bacillus subtilis genome containing the jic and celloci, and creation of a 177 kb contig covering the gnt-sacXY region.";

Microbiology 142:3113-3123(1996).

-! FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM, MOTILITY, SECRETION OR DIFFERENTIATION.

-! SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED INTO THE MEDIUM.
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OR 32 (POTENTIAL).
WALL-ASSOCIATED PROTEIN.
3 X 101 AA APPROXIMATE TANDEM REPEATS.
1-1.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=168 / BGSC1A1;

MEDLINE=95219088; PubMed=7704263;

Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;

Yoshida and sequenching of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci.";

Microbiology 141:337-343(1995).
                                                                                                                                                                                                                                                                              "Molecular analysis of three major wall-associated proteins of Bacillus subtilis 168: evidence for processing of the product of gene encoding a 258 kDa precursor two-domain ligand-binding
                                                                                                                          Bacillus subtlis.
Bacieria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                  (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 41, Last annotation update)
                  2334 AA
                PRT;
                                                                                                      Wall-associated protein precursor.
WAPA OR N17G.
                                                                                                                                                                                                                             STRAIN=168;
MEDLINE=93302506; PubMed=8316082;
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EMBL; 299124; CAB15959.1; -...
Subtilist; BG10797; waph.
InterPro; IPR003305; CBM Cenc.
Pfam; PF02018; CBM 4 9; I.
Cell wall; Repeat; Signal; Compl.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                  Mol. Microbiol. 8:299-310(1993).
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                   STANDARD;
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                                    Q07833;
01-OCT-1994
                                                                      01-OCT-1994
15-JUN-2002
                   WAPA BACSU
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HGBC HABIN
Q9KIVO;
16-OCT-2001
                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=NTH1 N104;
MEDLINE=20316037; PubMed=10858226;
Cope I.D., Hrkal Z., Hansen E.J.;
"Detection of phase variation in expression of proteins involved "Detection" of phase variation binding by nontypeable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2182
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                                                    EMBL; AF221060; AAF80178.1; -.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
                                                                                                               use by non-prefit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                            the
                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
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                                                                                                                                                                                                                                             IS REQUIRED FOR HEME UPTAKE.

IS REQUIRED FOR HEME UPTAKE.

SUBCELLULAR LOCATION: OUTER membrane.

MISCELLANEOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAA REPEAT REGION. THIS MECHANISM IS CALLED SLIPPED-STRAND MISPAIRING. ADDITION OR LOSS OF CCAA REPEAT UNITS WOULD CHANGE THE READING FRAME AND RESULT IN INTRODUCTION OF STOP CODONS DOWNSTREAM OF THE REPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION AND A WAY TO AVOID THE IMMUNOLOGICAL RESPONSE OF THE HOST.

SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY;
                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                       HEMOGLOBIN/HAPTOGLOBIN BINDING PROTEIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN
                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTPE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKYFYHYNAHGDIIAISDSTGKTVAKYQYDAWG----NPTKTEASDEVKDNRYRYAGYQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |:| | | | | KETHEDGTVIEYTYDG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDPDGHWVWLVVNAGFAAYDGYKAYKSGKGWKGAAWAAASNFGPGKIFKGASRAYKFTKK
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                                                                                                                                                                                                                                                                                                                                                                                                                         Immun.
PS00430; TONB DEPENDENT REC 1; FALSE NEG.
PS01156; TONB_DEPENDENT_REC_2; 1.

Rbrane; Transport; TonB box; Multigene family; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteobacteria;
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(Rel. 40, Last seq
(Rel. 40, Last ann
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40, Last annotation update)
g protein C precursor.
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Best Local
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                                          PAT2 HUMAN STANDARD; PRT; 4349 AA QNYYÖB; O75091; QNNSR7; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Protocadherin Fat 2 precursor (hFat2) (Mult factor-like domains 1).
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REPEAT
REPEAT
REPEAT
SITE
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SIGNAL
CHAIN
            FAT2 OR MEGF1 OR CDHF8.
Homo sapiens (Human).
Eukaryota; Metazoa; Cho
                                                                                                                                          MAMDH
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                           EGNA-TYGYIGKWRESELETEVLNGRKFARIKDRK-----DKNNRDNR
                                                                                                                                                                                                                                             Q--FKEKGTAADGTKTYDFDTFIDTNNQEIVGKLNLGYANDTWYDCSLFDCKDGTKMKVF
                                                                                                                                                                                                                                                                     HKASKTKFTGYAGA-VYDLN-----DNNSLYLSLSQLYTPQTNLDA------DGKLLKPR
                                                                                                                                                                                                                                                                                                                          VR------GYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTL
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                                                                                                                                                                                                                                                                                                TRARTDEYCDAGVTHCQGTEN------PTGLKLTNG-----KITRRNGTDL
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256
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HEMOGLOBIN BINDING PROTEIN C.

X 4 AA TANDEM REPEATS OF Q-P-T-N.
Craniata; Vertebrata; Catarrhini; Hominidae
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NB C-TERMINAL BOX.

A551BF3B2C641612
                                                             (Multiple
                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ENYDYKNADS
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 Hominidae;
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                                                               epidermal
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            Euteleostomi;
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                                                             growth
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CADHERIN 15

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                                                                                                                                                                                                         SEQUENCE OF 3777-4349 FROM N.A.
TISSUB-Brain;
MEDLINE-98360089; PubMed-9693030;
Nakayama M., Nakajina D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple
EGF-like motifs by motif-trap screening.";
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R Genew; HGNC:3596; FATZ.

R MIM; 604269; -.

R HSSP; P00740; IEDM.

R HSSP; P00740; IEDM.

R INTERPOO; IPR002126; Cadherin.

R InterPro; IPR001791; Laminin_G.

R InterPro; IPR00028; EGF-like.

R PRINTS; PR00028; EGF, 2.

R PRINTS; PR00028; EGF, 3.

R SMART; SM00112; CA, 32.

R SMART; SM00181; EGF, 3.

R SMART; SM00181; EGF, 3.

R PROSITE; PS00282; LamG; 1.

R PROSITE; PS00282; CADHERIN 1; 14.

R PROSITE; PS01286; EGF 2; 1.

R PROSITE; PS00186; EGF 2; 1.

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R PROSITE; PS0025; LAM_G DOMAIN; 1.

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                                                                                             Wu O., Maniatis T., "Large expose ancoding multiple ectodomains are a characteristic feature of protocadherin genes "; Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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CADHERIN 13.
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MEDLINE=20202599; PubMed=10716726;
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Uchida M., Tanaka H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0014; FNTYPEIII.
PRODOM; PD000471; Glyco_hydro_18;
SMART: SM00495; ChtBD3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00495; ChtBD3;
SMART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00704; Glyco_hydro_18; Pfam; PF02839; CBM_5_12; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interPro;
                      663
                                           546
                                                                613
                                                                                       486
                                                                                                             574
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                                                                                                                                                        548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , M57601; AAA815
A38368; A38368.
                                                                                                                                                                                                   KFTGYAGAV-YDLNDNNSLYLSLSQLYTPQTNLDADGKLLKPRQGNQFEVGYKGSYMDDR
                                                                                                                                                                                                                                                                        DA----
                                                                                                                                                                                                                                                                                                                                                               GKKYL----LTIASGASATYAANTELAKIAAIV----DW---
                                                                                                                                                                                                                                                                                                                                                                                                           EYPVSGGLD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 EADVSGSLNSDGSVRGRVMAQTVGASPRPAEKNNR-----HETFYAAADWDINPDTVL
TGTTATISGLAADTSYTFTVKAK--DAAGNVSAASNAVSVKTAAETTNPGVS-AWQVNTA
                     AGGYATFDAMAA---YRFTPKLKLQINADNIFNRHYYARVGGANTFNIPGSERTWTANLR
                                           TVSTTAQPGGDTQAPTAPTNLASTAQTTSSITLSWTASTDNVGVTGYDVYNG
                                                                TASNSRDDGIFLLMPKHSANLWTTYQVTPELTIG------
                                                                                       NASTDNVGVTGYNVYNGANLATSVTGTTATISGLTAGTSYTFTIKAKDAAGNLSAASNAV
                                                                                                            ----RYAALGKRVMEG--VETEISGAVTPKWQIHAGYSYLH-----
                                                                                                                                 GLGGAMFWELSGDRNKTLQNKLKADLPTGGTVPPVDTTAPSVPGNARSTGVTANSVTLAW
                                                                                                                                                        RYWNDTAKVPYLYNASNKRFISYD-----DAE----
                                                                                                                                                                                                                                                 RKGVRGYSHTVATENLDEFGIYGKSTFHPADGLSLIGGGRLGHYKIESGEGKTLHKASKT
                                                                                                                                                                                                                                                                                            DASYSRPFRIGHTANEFVIGADYNRFRSTNEQGRTTLYARGGLALNEFRSIPQVDLIANA
                                                                                                                                                                                                                                                                                                                    GAWQKI ---
                                                                                                                                                                                                                                                                                                                                        GGYGKVGMRYSDRDADSNYAFAGSKLGMKTPAGRPGCNTADDKACAVGLGTEIKQKALAF
                                                                                                                                                                                                                                                                                                                                                                                    GAGYLYQQRHLAPYNGLPAD--ANNKLPSLPQHVFVGADWNKFKWNSHDVFADLKHYFGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o; IPR003610; CBM 5_12.

j; IPR001579; ChiTinase 18/2.

j; IPR003961; FN III.

j; IPR003962; FnIII_repeat.

j; IPR001223; Glyco_hydro_18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS01095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465
2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1FNA
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                                                                                                                                                                                                                                                                                                                 -SAHNAPLNYDPAAS-----AAGVPDANTFNVAAGAQG------HL: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÃĂ;
                                                                                                                                                                                                                                                                       GVPAAKLVLGVPF---
                                                                                                                                                                                                                          ------GNGQYQTCTGGSSVGTWEAGSFDFYDLEANYINKNGYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHITINASE 18; 1. idase; Chitin degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  699
460
549
644
204
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73677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW.
                                                                                                                                                                                                                                                                                                                                                                                                           --GNSKRPEDKQNYTLLLSKIREKLDAAGAVD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 129; DB
Pred. No. 0.26
47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHITINASE A1.
CATALYTIC.
FIBRONECTIN TYPE-III (R-1
FIBRONECTIN TYPE-III (R-2
PROTON DONOR (PROBABLE).
D->N: DECREASE IN ACTIVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D->E: NO CHANGE IN ACTIVITY E->D, Q: LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC7C9B22E2987643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DECREASE IN ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Repeat
                                                                                                                                                                               ----SVGYKTAYIKSK
                                                                                                                                                                                                                                                                                                                                                              -----INIMTYDEN
                                                                GGVNAMSGITSSAGMH
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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(R-2)
                                           -TALATTV
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                                                                                                                                                                                                                                                                      DGCAQA
                                                                                                            SQIK
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                                                                                                             612
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161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -: SUBCELLULAR LOCATION: OLDER membrane.
-: SUBCELLULAR LOCATION: OLDER MEMBRANE.
-: MISCELLANBOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE
EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAA
REPEAT REGION. THIS MECHANISM IS CALLED SILPPED-STRAND MISPAIRING.
ADDITION OR LOSS OF CCAA REPEAT UNITS WOULD CHANGE THE READING
FRAME AND RESULT IN INTRODUCTION OF STOP CODONS DOWNSTREAM OF THE
REPEAT REGION. THIS MAY BE A MECHANISM OF TREGULATION AND A
MAY TO AVOID THE IMMUNOLOGICAL RESPONSE OF THE HOST.
-: SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY;
HENGGLOBIN/PAPTOGLOBIN BINDING PROTEIN SUBPAMILY.
-: CAUTION: THIS IS A CONCEPTUAL TRANSLATION, A FRAMESHIFT WAS
INTRODUCED IN THE REPEATS REGION TO MAXIMIZE THE SIMILARITY
WITH OTHER ORTHOLOGS.
                                                                                                                                                                                                                                                                                                                                                  "Identification of an outer membrane protein involved in utilization
                                                                                                                                                                                                                                                                                                                                                                                                                                      Coudert E.;
Unpublished observations (AUG-2001).
-!- FUNCTION: ACTS AS A RECEPTOR FOR THE HEMOGLOBIN/HAPTOGLOBIN
COMPLEX OF THE HUMAN HOST AND IS REQUIRED FOR HEME UPTAKE. DOES NOT BIND HEMOGLOBIN ALONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEMOGLOBIN-HAPTOGLOBIN BINDING PROTEIN
                                                                                                                                                                                                                                                                                          STRAIN=NTHI TN106;
MEDLINE=96355882; PubMed=8751920;
Maciver I., Latimer J.L., Liem H.H., Muller-Eberhard U., Hrkal Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X 4 AA TANDEM REPEATS OF Q-P-T-N.
                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemoglobin-haptoglobin binding protein A precursor (Hemoglobin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, U43198; AAB36696.1; ALT SEQ.
InterPro; IRR000531; TonB_boxC.
Pfam; PF00593; TonB_boxC; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
Outer membrane; Transport; TonB_box; Multigene family; Signal;
                                                                                                                                                                                                                                                                                                                                                                 hemoglobin-haptoglobin complexes by nontypeable Haemophilus
                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
NCBI_TaxID=727;
                                                                                               1046 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                               PRT;
                                                                                                                                                                               haptoglobin utilization protein A)
                                                                                                                                                                                                                                                                                                                                                                                         Infect. Immun. 64:3703-3712(1996)
                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                          Haemophilus influenzae
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
33
38
38
                                                                                                                                                                                                                                                                                                                                                                              influenzae.";
721
                          663
                                                                                               HHUA HAEIN
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720 YS
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REPEAT
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REPEAT
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HAEIN
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RVL-SNDDGRSSVYARGYEYSE--YNIDGLPAQMQSINGTLPNLFAFDRVEVMRGPSGLF 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 DARDYLLINKNYYASYKRGYNTAD-NQNLQTLTLAGRYKY------FDAIAVITS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387 IGADYNRFRSTNEQGRTTLYARGGLAL--NEFRSIPQVDLIANARKGVRGYSH----TV 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:: |:: |:: |:: | 361 RIDDYCDGNDKCALAGNPL----GMKYNQDNQLVGEDGNLAKYK-DINTKQTIHEKLPF 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                         44 YNAIVTEKNGDYSSFAVTVGTKIPASLREIPQSVSIITNQQVKDRNVDTFDQLARKTPGL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 EGYGNFNNTRN------TAEIETLKQVTIRKGADSLKSGSGALGGSVSFDTK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GASPRPAEKN--NRHETFYAAADWDINPDTVLGAG-YLYQQRHLAPYNGLPADANNKLPS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPQHVFVGADWNKFKMNSHDVFADLKHYFGNGGYGKVGMRYSDRDADSNYAFAGSKLGMK 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 TPAGRPGCNTADDKACAVGL-GTE-----IKQKALAFDASYSRPFRLGNTANEFV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 REKADPYRRTQESKLLKFAFQPTENHRLSVVVDLYKQTSKGHDFSYTLK----ONTEH--- 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 ATENL----DEFGIYGKSTFHPADGL-----SLIG-GGRLGHYKIESGEGKTLHK---- 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ASKTKFTG---YAGAVYDLNDNNSLYLSLSQLYTPQTNLDADGKL 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 TKPNEKWRYNRVDWDALKKKYPGVPIYASCIEENND--------PSKYCSYDVEI 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               527 LKPRQGNQFEVGYKGSYMDDRLNARVSFYRMKDKNAAAPLN--PNNKKTRYAALG----K 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PKKENTFEINGK-------OYDLLSEADKNVISDEQRLPTNSSYLFSCDGLNCDK 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTFD STRMU STANDARD; PRT; 1462 AA.
P49331; 069383; 069386; 069389; 069398;
01-FEB-1996 (Rel. 33, Created)
15-ULL-1999 (Rel. 38, Last sequence update)
15-ULL-1999 (Rel. 38, Last annotation update)
Glucosyltransferase-S precursor (EC 2.4.1.5) (GTF-S) (Dextransucrase)
                                                                                                                                                                                                                                                                                                               61 HNDNTPPK-----IAETIKT---AKKPEKEQA------QDVKD------LVRYETGI 97
                                                                                                                                                                                                                                                                      5 MSVFRINMTAATVLAALSSSV-FAAQ------TAQ---TADLETVHIKGQRS 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQYPHSCDIFLPSSTPN-----GAPTLN---PERTNTLCNNSNV-YSF 660
                                                                                                                                         3.4%; Score 129; DB 1; Length 1046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAYRFTPKLKLQINADNI FNRHYYARVGGANTPNI PGSERTWT----ANLRYSF
51 58 TONB BOX.
1029 1046 TONB C-TERMINAL BOX.
1046 AA; 119295 MW; ASD208A68D27A84E CRC64;
                                                                                                                                                                                                    271;
                                                                                                                                                                  21.1%; Pred. No. 0.46; ive 97; Mismatches
                                                                                                                                                                                                           Conservative
                                                                                                                                                                     Best Local Similarity
Matches 176; Conserv
                                                                    SEQUENCE
                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 45
GTFD STRMU
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REMBL; M2926; AAA26895.1; -.

REMBL; D88653; BAA26107.1; -.

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Kimura S., Hamada S.;
"Molecular analyses of glucosyltransferase genes among strains
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FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
CATALYTIC ACTIVITY: Sucrose + {(1,6)-alpha-D-glucosyl}(N) = D-fructose + {(1,6)-alpha-D-glucosyl}(N+1).
SUBCELLULAR LOCATION: Secreted.
DISEASE: DENTAL CARLES.
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